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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	63771	029	X96471 C.glutamicu	APSSSS Sequence z APO05277 Corvnebac	AX127147 Sequence	AX123539 Sequence	AL646059 Ralstonia	AL357613 Streptomy	AEU04852 PBeudomon AE008841 Salmonell	AE005522 Escherich	AP002563 Escherich	U65741 Aeromonas s	AX030085 Sequence	E49392 Process for	X14436 Escherichia	U28377 Escherichia	AL646067 Ralstonia	U34849 Mycobacteri	AE007056 Mycobacte	186263 Sequence 17 Z74025 Mycobacteri	AE009057 Agrobacte	AE008023 Agrobacte AE006952 Mycobacte	Z77162 Mycobacteri	AE013931 Yersinia	AD414145 IEFSINIA AE011957 Xanthomon	AB011413 Streptomy	AE009566 Brucella AE004134 Vibrio ch	69 Aeromona	ACI05744 Oryza sat	9315 F	32557 5	97204	P005610 C		Ē	iinedi FAI 24-JAN-2001			a, Actinobacteridae; Corynebacteriaceae;		Zelder,O. and Haberhauer,G. ng metabolic pathway
SUMMARIES	ar	AX063771		CGLYSEG	AP005277	AX127147	AX123539 AB083133	AL646059	SCSF8	AE008841	AE005522	AP002563	ASU65741	AX030085	E49392	ECFDAPGK AROOO375	ECU28377	AL646067	MBU34849	AE007056	I86263 MTCY39	AE009057	AE008023 AE006952	MTCY20G9	AE013931	AE011957	AB011413	AE004134	AHAHYGENE	ACI05744	AF429315	••	AC097204	99	ALIGNMENTS		ent WO0100843.	483	glutamicum.	nobacteria; terineae; Co		,B., Schroeder,H., Zel amicum genes encoding
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RVPIGGYGAQYGDTGWIFPAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVV
AVVMTALAIKLMILMG"
                                                                                 PAT 28-SEP-2001
                                                                                                                                                                                                                                                                                                                                           Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O., Haberhauer, G., Kim, J.W., Lee, H.S. and Hwang, B.J.
Corynebacterium glutamicum genes encoding metabolic pathway
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101_.802
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                                                                                 DNA
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BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
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FVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSFKVWRWINVVV
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100.0%; Score 711; DB 6; L
Best Local Similarity 100.0%; Pred. No. 2.5e-168;
Matches 711; Conservative 0; Mismatches 0;
proteins
Patent: WO 0100843-A 53 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
                                                                                                     1. .822

| Organism="Corynebacterium
| Ab_xref="taxon:1718"

101. .802

| Note="RXA01394"
                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
/protein_id="CAC25127.1"
/db_xref="GI:12541484"
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Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
1. .2374
/organism="Corynebacterium glutamicum"
                                                                                                                                                                                                                                                                                                                                                         cellular function:
                                             600
                                                                                        99
   540
                        631
                                                                  691
                                                                                                              751
                                                                                                                                                                                                                                                    lysE gene; lysG gene; Lysine export regulator protein; Lysine exporter protein; Lysine governor.
Corynebacterium glutamicum.
Corynebacterium glutamicum.
Bacteria; Firmicutes; Actinobacteridae;
Actinomycetales; Corynebacterinaces;
                                                                                    GCAGCAGCATTGTCACGCCCGGTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                        692 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTCGATCAACGTCGTC
                   572 TIGGACGCGIIIIGIGIIIIAICGGCGCGCGCGCGCGCAAIACGGCGACACCGGACGGIGG
                                           ATTITCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCCGCTGGTGGGTTTCGGC
                                                                                                                                                      802
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                                                                                                                                             GTGGCAGTTGTGATGACCGCATTGCCATCAAACTGATGTTGATGGTTAG
                                                                                                                                GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAG
                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 2374)
Vrljic,M., Sahm,H. and Eggeling,L.
A new type of transporter with a new type of cel
L-lysine export from Corynebacterium glutamicum
Mol. Microbiol. 22 (5), 815-826 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/product="Lysine exporter protein"
/protein_id="CAA65324.2"
                                                                                                                                                                                                             DNA
                                                                                                                                                                                                       C.glutamicum lysE and lysG genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Lysine governor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:1718"
complement(82..954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (82. .954)
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transl_table=
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/gene="lysE"
1025. .1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="lysG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="lysg"
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                                                                                                                                                                                                                                          X96471.1 GI:1729753
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                                                                                                                                                                                                                                                                                                                        Corynebacterium.
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ACCESSION
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PUBMED
REFERENCE
AUTHORS
                                                                                                                                661
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TITLE
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/db_xref="GI:13397387"
/db_xref="SWISS-PROT:P94633"
/tcmanslation="MEIFITGLILGASLLLSIGPQNVLVIKQCIKREGLIAVLLIVCLI
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ETEPTVPDDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDA
RVPTGGYGGAQYGDTGRNIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVV
AVVPMTALAIKLAMLMA

ÇOOMDlement (1723. . 2352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MYALRDIVASGKALYVGISSYGPELTAEAABFWAEEGCPLLIHQ
SRSTINWWEBEPGDGERALLÓSAAAMGLGVTAFSPLAQGLITDKYLDGIPEGSRASQ
GRSLSEGEMLAVNNIDHWYRKLADIAQERGGSLAQWALAWVLREGGEYGADTYTSALIGA
SSVEQLDNSLDSLANLEFSDAELEAIDEISHDAGINIWAKATDSKTREN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTITICGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTTGGGTTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1556 ATTTTCGCCGCTGGCGCGTTCGCCGCAAGCCTGATCTGGTTCCCCGCTGGTGGGTTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCTTCTCGTGTGTTTAATTTCTGACGTCTTTTTTGTTCATCGCCGGCACCTTGGGCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 711; DB 1; Length 2374; 100.0%; Pred. No. 2.8e-168; tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALKODKAFRRFYLVRSMITVTALSTAFIVALAAESGNSIDSLGFFIIASGLAGMYGG
RISGIWSDHSSKNVMAGGALFGSIVLILVVLSSAFAPAQINTLVFPLSFFIITLAHTA
IRVARKTYVMDMAEGDQRTRYVADANTLMGVVLLIVGALSGFIAIFGNEAALLFLAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTGLHAYRGLAGMI IVEDEATDKLDLPREYGVDDI PLVLMDHRFLEDGSLDEEDLPDL
GLLGDTPTANGITNAHFDATTRRVRFRVLNGSNMRFYNLAFSDTRTFQVIASDSGLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPQDRTTLAIGPGERWEIVVELEPGEDVTLESVGFEDNYGVPDDEFVPDFGMSDSFQL
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HDQPEVWIVTNDNSDWPHNFHVHDARFKVLKFEGTDVELFNDGWKDTVGLPPGATATL
                                                                                                                                                                                                                                        AP005277 333150 bp DNA linear BCT 08-AUG-2002 Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVINNLDEMTTVHWHGMKL.PAIADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MTNPTEERNARRLIWANGLONIGDOIVAAKTVLPWLLOAAGAPG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MPELNRRTFFKGAGVLAATVVGAQVLVACSSDDVRGYGGEPRTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIPPADLGTREGSSVHFALEAQTGESQILPDVTTKTWGFNGTHLGPTLVVKKGDDVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,
Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo
Co. Ltd. And Kitasato University.
Location/Qualifiers
1. 333150
                                                                                                                                                                                                                                                                                                                                                                                   (strain:ATCC 13032) DNA
                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum ATCC 13032 (strain:ATCC 13032) DNU Corynebacterium glutamicum ATCC 13032 Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Corynebacterineae; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Corynebacterium glutamicum ATCC 13032"
                                                                                                   GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGTTAG 1726
                                                                        711
                                                                        GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical membrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB98338.1"
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AP005277.1 GI:21323710
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/transl_table=
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KEYWORDS
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AP005277/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1556 ATTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCGGTGGGTTTCGGC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1016 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGCCCAGTCTTTTACTGTCC 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1136 Grichrichengrinahrrichgaegrichringrichreecegeaechreegeerr 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACAGATCATTGAAGAAACAGAACCGAGCCCGATGACACGCCTTTGGGCGGTTCG 360
                                                                                                                                                                                                                                                                                                                                                                                                         BOOSTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTAT
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                                                                                                                                                                                                                                                                                                                             Corynebacterium.

1 (bases 1 to 2174)

1 (bases 1 to 2274)

Vilic,M. and Eggeling,L.

PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY ACTIVITY OF EXPORT CARRIERS

Patent: WO 9723597-A 2 03-JUL-1997;

KERNFORSCHUNGSANLAGE JUELICH (DE); VRLIJC MARINA (DE)
                                                                                                                                                                                                                                                                                    a, Actinobacteridae,
Corynebacteriaceae;
1676 GIGGCAGTIGIGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAG 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 711; DB 6; Length 23
100.0%; Pred. No. 2.8e-168;
ive 0; Mismatches 0; Indels
                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 2374
/organism="Corynebacterium glutamicum"
/db_xref="taxon:1718"
640 c 648 g 560 t
                                                                                                                         DNA
                                                                                                                                                                                                                                    Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria, Firmicutes, Actinobacteria,
                                                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae;
                                                                                                                    A93933 2374 bp
Sequence 2 from Patent W09723597.
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                                                                                                                                                                                          GI:6742037
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Best Local Similarity 100.
Matches 711; Conservative
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DPSNRTDVCVLDLQLGGIDGIDTATRLMBTTPDLAVLIVTSHARPRQLKRALAAGVLG
LPKTSTADBERTALRTVHAGRRYIDPBLAAMTISAGESPLTRREBEVLELAGGGLSA
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complement (6781. . 6987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MKHYWSMYPGAGPLNTPHTKEVWFMDIVSIVNHWFEWSTNNWVN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LASDSTEILNLVRDEVNQYVPEDQSHVVNGVIDSIAGSAAAGQVGVAVGVITALWTSS
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APIAEPLHLTNVLSPLTDRFMPIMIWVRFPVIVGVLIMFVATLYYMAPNARPWKFRWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="wtawicsfpsgyodbydmwngvvqpqehidatilaadfhgnpen
sgdrkerinfqgwkyyalnrtvrdvffdglidlaalliffsilsiapavilgysvitif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLLVLVLVPI I SGVVALASKGI SKRSVTQQEKLAESGAQASDIMMGLRVI KAIGGERW
AVKTPEKASQASARAAVDTAVASGKVAGIGELSIAVNLAAVLLLAGWRVTTGELGPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIAIVGVAVYLSEPIRLLSNSINASAIAHGAAERVANFLNLDESQAQYESSETINDGE
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IKQLRAGKTTIVVSSSPAFYNLADRVISHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:21323719"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLIVDHAVLTKDLRRLVVGLVAFVVLFVVLSFSYRFGSRALNRAVNFESHALRVEVAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transI_table=11
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system, ATPase component"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEISRAKQLQAGMPAEDYSLVPPRSIEKVAKMKQRQQRLMDQAAAIREESN"
                                                             /product="Two-component system, response regulators consisting of a CheY-like receiver domain and a HTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTTGGGGGCCAGTCTTTTACTGTCC
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8672. 10114
/gene="Cg10952"
/gene="Cg10952"
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PF00664:ABC transporter transmembrane region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="tRNA-processing ribonuclease BN"
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100.0%; Pred. No. 5.5e-168;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein"
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/db_xref="GI:21323717"
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                                                                                                                 DNA-binding domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTGLPRETFVPAFVGSTVLAVLSF
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/gene="Cg10950"
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7048. .8205
/gene="Cg10951"
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                                   table=11
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/transl_table=
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Matches 711;
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AVEPGHYPDPQWPYMYHCHMLYHEDQGMMGQFVIVEPGDEPAAVLGSGTGSSIDSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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CSALALMTSGFTRNASAAQMTSMPVFWLAMGGLGSIRFVFGDSIVADILAYTPFAJIS
DLVQIGWAGATFADSVGGVEAANFAGIFQDMLIPLGAMTPAAAVWAANRYWRWDSY
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RRIEASLRVTERRIRRAQELHDTLGQHLAANGVVIPPLMAGTVRLSVWTVDVMKEVERS
RELEASLRVTERRIRRAQELHDTLGQHLAANGVKSELALALAKRGDDRLENELRELQK
LIRTSMSERRDVSGYRTVNLATEIERSKSLLADAHIHLSVIGTTSQVSPAHRELCAW
LVRRATINILARSDATTLTLSSTEVRMDNKGVNKDIGRLSGLSALRSRAESAGMTL
IVSREDDQFSVRMLINAPANTPAEKKA"
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TGLDPESRRHTWQLLLDLKQRGVTWMLTTHYLERAEFICDRIAIMNAGEIAVEGTLDB
LVAREKSIISFVLRGGQVELLYLSGAEIIRDNNHVRIATTTLQQHTLEILTWAAETGI
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TRVSLQAIPVVLLSAXFLGIVANAGTLNPSFVWLLGFSVILLIVTVLVYEYQPSLNS
                                                                                                                                                                                                                                                                                                                                                                       O
                                                                                                                                                          /note="PP00005.ABC transporter
TIGR00960:3a0501802: Type II (General) Secretory Pathway
(IISP) Family protein
TIGR00968:3a0106801: sulfate transport system permease
                                                                                                                                                                                                                                                                                                                                                           TIGR01184:ntrCD: nitrate transport ATP-binding subunits
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR01186:prov: glycine betaine/L-proline transport ATP binding subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICR01188:drrA: daunorubicin resistance ABC transporter
ATP-binding subunit
TICR01189:ccmA: heme exporter protein CcmA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIGR01187:potA: spermidine/putrescine ABC transporter
                                                                                                                                                                                                                                                                               protein
TIGR01166:cbiO: cobalt transport protein ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transI_table=11
product="ABC-type transporter, permease components"
protein id="BAB8340.1"
db_xref="GI:21323714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="Two-component system, sensory transduction
istidine kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PF00072:Response regulator receiver domain
PF00196:Bacterial regulatory proteins, luxR family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEGFAAKPATLESVFMDIASLENTSLQTA"
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codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding subunit
                                                       .063. .3983
gene="Cg10946"
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|gene="Cg10947"
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/gene="Cg10947"
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gene="Cgl0948"
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gene="Cg10948"
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                                                                                                                                      gene="Cg10946"
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transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
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PAT 11-MAY-2001
                                                                                                                         Db 128953 AIGGIGAICAIGGAAAICTICATIACAGGICTGCTITITGGGGGCCAGICTITIACIGICC 128894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128593 GCGGTGGCCACTGACACCGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128533 GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128773 GATCTTTTGTCCAATGCCGCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 128653 CCACAGATCATTGAAGAAACAGAACCAACCGTGCCCGATGACACCCTTGGGCGGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128353 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                                                                                                                                                          ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG
                                                                                                                                                                                                                                                                                                                  TTGGACGCGTTTGTGTTTATCGGCGCGTCGGCGCGCAATACGGCGACACCCGGACGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 ATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
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1 (bases 1 to 708)

Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polynucleotides
Patent: EP 1108790-A 3455 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128293 GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGTTAG 128243
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Corynebacterium glutamicum
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
Actinomycetales, Corynebacterineae, Corynebacteriaceae;
                                                                                      1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTTGGGGGCCAGTCTTTTA
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                                   Indels

    . 708
    /organism="Corynebacterium glutamicum"

     100.0%; Pred. No. 5.5e-168;
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                                   0; Mismatches
                                      711; Conservative
  Best Local Similarity
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                   Matches
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                            Db 128893
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                                Db 328943 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAAGCGCGAAGGACTCATTGCG 328884
                                                                                                                                                                                                                                                                              Db 328823 GATCTTTGTCCAATGCCGCCCGATCGTCGTCGATATTATGCGCTCGGGTGGCATCGCT 328764
                                                                                                                                                                                                                                                                                                                                                                        DD 328703 CCACAGATCATTGAAGAAACAGAACCGACGCCCGATGACACGCCTTTGGGCGGTTCG 328644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGACGCGTTTGTTTTTTCGCCGCGTCGGCGCGCATTACGGCGACCGGACGGTGG 328464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 328463 ATTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC 328404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 328403 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTCGATCAACGTCGTC 328344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 328643 GCGGTGGCCACTGACACGCGCAACCGGGTGGGGGTGGAGGTGGAGCGTCGATAAGCAGCGCG 328584
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/organism="Corynebacterium glutamicum"
/db_xrefe"taxon:1718"_
/not=refe"5eq 1 to long (3.309.400) split in 11, seq 7063
1.200.001 1.549.980"
80727 a 91049 c 97618 g 80586 t
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**Recorynebacterium glutamicum
Bacteriu; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterium:
Corynebacterium:

**Audo, S. Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.

**Novel polynucleotides
Datent: EP 1108790 Co., LTD. (JP)

**Extent of the control of the c
                                                                                                                 GTTCTTCTCGTGTGTTTAATTTCTGAGGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTT
                                                                                                                                                       Db 328883 GTTCTTCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGCACCTTGGGCGTT
                                                                                                                                                                                                                                  GATCTTTTGTCCAATGCCGCGCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
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128474

480

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128534

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360

128294

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Procein id="BAB88826.1"

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PPPPVBAEVAHWGAVTTLRVEDEAHTLSLLRRGSVLGAVTREADPVAGCEVLRLGVMR

HLPVATPELRARYTVDGQPDWVRMPVLRFGENDVLQDRDLEGRVDGAVARRRVSVVPS

AEGFGEAVRLGLGWGLLPEAQAAPMLAAGDVVQLDEKVVDTPLYWQRWRLESRLLARL
Published Only in Database (2002)

2 (bases 1 to 1771)

1 (larga.H., Kimura.E., Kawahara,Y. and Sugimoto,S.

Diract Submission
Submitted (04-APR-2002) Hiroshi Itaya, AJINOMOTO CO., INC,
Fermentation & Biotechnology Laboratories; 1-1, Suzuki-Cho,
Rawasaki-Ku, Kawasaki, Kanagawa 210-8681, Japan
(B-mail:hiroshi itaya@ajinomoto.com, Tel:81-44-244-7123(ex.4146),
Pax:81-44-222-0129)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TACCTGTTATGGTTTGCCGTCATGGCAGAGACGCCATGACAACAACAAGGTGGAAGCG 300
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/product="Lysine export transcriptional regulatory
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/organism="Corynebacterium efficiens"
/db_xref="taxon:152794"
complement(47. .919)
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Pred. No. 3.1e-69;
0; Mismatches 214;
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/gene="lysE"
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/gene="lysE"
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llarity 67.7%;
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Corynebacterium efficiens
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                     ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGGAAGGACTCATTGCG
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                                                                                             Length 708;
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lysG, lysE of Corynebacterium efficiens
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                                                                                        Query Match 99.6%; Score 700; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 708; Conservative 0; Mismatches 0;
                        180
  db xref="taxon:1718"
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston
Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie
Moleculaire des Interactions Plantes-Microcyganismes INRA-CNRS,
BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean
Dansset-CRH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS
I18 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA
URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France,
Laboratoire de Biometrie et Intelligence Artificialle INRA, BP27,
F311326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
INRA, BP27, F31326 Castanet-Tolosan Cedex
Christian.Boucher@coulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2001
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Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S.,
Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolioo, L.,
Chandler, M., Choisne, N., Claudel-Renard, C., Cunnac, S., Demander, M., Golsne, M., Robert, C., Saurin, W., Schiex, T.,
Siguier, P., Thebault, P., Mhalen, M., Mincker, P., Levy, M.,
Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                              1326 GGCGGGGCGTGACGACGACGACCCCCGGCTCCGCATCACATCAGGCACCCGGCAG
                                                                                                                                         1386 Grendedrekadeceandereandeceangedendecendecendareceandecende 1445
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AL646059 AL646052
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                            GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTAT
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GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTCGATAAGCAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTA 710
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/gene="RSc0382"
/note="RS03350"
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/gene="RSc0382"
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AUTHORS
TITLE
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361
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AUTHORS
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DPDREPPFPPCKPADAVRYVADGTTGQFVYPTETRDCHYEIELVVAIGTGGRDIAVES
AAQHIYGYAIGLDMTRRDLQNAAKKGGRPWETGKAFDGSAPIGPIVPAQTVASPDRGA
ITLSVNDKAHQHGDLSDLIWSVPETIAYLSRLFELRPGDLIFTGTPEGVGPVSIGDLM
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CEIHPLNNPRVLKYLKHTFNVGDDARNDMYRHWVRLGFAALETRLTQSPRTGACCVGD
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PEAIVDGIKPTRVALDVAYARFEHERALABLDNAKTQLAERKVLERAKGLLMQQM
QLSEDBAFKRLRKWAMDRNIKLVEAAQRVIDVWAG"
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/function="small molecule metabolism; degradation; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          937. .1638
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//gene="RSc0383"
/function="miscellaneous; hypothetical/global homology"
/function="miscellaneous; hypothetical
Gene name confidence : hypothetical
Gene name Confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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/note="Product confidence : probable
Gene name confidence : hypothetical
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/transl_table=11
/product="PROBABLE RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN"
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GUTATHINE TRANSFERASE ZETA 1) PROTEIN"
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Gene name confidence : hypothetical
predicted by Codon_usage
/note="Product confidence:
Gene name confidence: hypoi
predicted by Codon usage
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predicted by FrameD"
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/db_xref="GI:17427392"
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predicted by FrameD"
/codon_start=1
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/gene="RSc0384"
/note="RS03352"
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/gene="RSc0384"
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/gene="RSc0385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RSc0383"
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                                                                                                                                         /codon_start=1
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predicted by P
predicted by F
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2542

446

206

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 12-MAY-2002
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ALI357613.2 GI:20520783
amino acid decarboxylase; anti-sigma factor; integral membrane protein; LuxR-family regulator; LysR-family transcriptional regulator; membrane transport protein; oxidoreductase; regulatory protein; RNA polymerase sigma factor; serine/threonine protein kinase; stress-inducible protein; TetR-family transcriptional regulator; thioredoxin reductase; threonine dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. (bases 1 to 33285)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D. A. set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2663 GCTGGCGCTGCTCAATCCGCACGTCTATCTCGACACGTGGTGCTGCTGCTGGCGC 2722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           989
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                                                                                                                                                                                                                                                                                                                                                                                 CGTGCTCGATATTATGCGCTGGGTGGCATCGCTTACCTGTTATGGTTTGCCGTCATGGC 266
                         /transl_table=11
Product="PUTATIVE ZINC PROTEASE-LIKE SIGNAL PEPTIDE
PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2603 CGAGCGCCTGCAGGCGCGCAACGGCGACAAGGCCTCGCATGCGCAGGTGCTGGCGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                  2423 cérécricaceracrierrarcracacerraracaacaricacerraarcacerrages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGCGCAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AGCGAAAGACGCCATGACAAACAAGGTGGAAGCCCCACAGATCATTGAAGAAACAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 AATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTCGGCGCGCAATACGGCGACACCGGACGGTGTTTTCGCCGCCTGGCGCGTTCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567 AAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2783 GTCGATCCTGTGGTTCTCGCTGCTGGGGTTCGGCGCACGCTGCTGGAGCCGGTGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTGGCAGTTGTGATGACCGCATTGGC
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                                                                                                                                                                                                                                                                     Length 190050;
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                                                                                                                                                                                                                                                                     Score 84.2; DB 1; Length 1
Pred. No. 3.4e-10;
0; Mismatches 263; Indels
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'evidence=not_experimental
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Streptomyces coelicolor cosmid 5F8.
                                                                                                      /protein_id="CAD13916.1"
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Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                     11.8%;
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                         Matches 242;
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Best Local S
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ACCESSION
VERSION
KEYWORDS
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RGAERLQARNGDKASHAQVLASALALSLINPHYYLDTVVLLCAIGGRYAMPANVAFAG
GAMCASILWFSLLGFGARLLEPVFARPVAWRVLDALIGAVMWAIALTLIMGG"
                                                                                                                                                 translation="MTGPGPESAPLIGAALSGFGLGASLIVAIGAQNAYVLRQGLRRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein id="CAD13914.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTALRDLI ELLHPLEKTMVLGRDQPTVIMIAGVNGAGKTTSIGKLCKHFQTYGGSVL
LAGGDPRABAREQLVI WGQRNNVTVNGGSGOBAAVI FDANBARARGID INVADTA
GRLPTQLHLMEELKYKVRVI GRAMATAPHETLLVI DANTGQNALAGVKAFDDALGITG
LIVYKLDGTAKGGILAAIARQRPVPVYFIGVGEQVEDLQPFSAREFADALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAALTGAKVGTSQADTHEYRLANGILRIJVKEDHRAPTVAHMWWTHAGSIDEHKGTTGV
AHMLEHWRKGTRAVGPGESRRVAALGGRENAMTTEDFTWYPQQIEKSHLADVMALE
ADRHALEHWRKGTRAVGPGESRRWALLGGRENAMTTEDFTWYPQQIEKSHLADVMALE
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AQDEEKQVGVKRIWKAPARNYAYANAYKAPPLRDVEKDVDPYALEVLSAVLDGYDNA
RLPHLLVKGKDEKGRLADVNAGYTGORNROFPSI FLLIGGYADGHTTFABT EQALRAQI
DRIAROGVTEARLKYKVAQVVAQIYKRDSYPGGGNEIGMABHTGISRRDLNRILEKI
KSYTPAQVQQVAKTYFTEDNLVVATLLPQPIDPNKPARRFVPGMREEGGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MRSFPQSVSNSARTGLRWAGITLAVALLAGEAGAQAPAPMAARQ"
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/function="miscellaneous; hypothetical/global homology"
/functe="Product confidence: putative
Gene name confidence: hypothetical
predicted by Codon usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /BC number="3.4.99."
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Gene name confidence : hypothetical
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Gene name confidence : putative
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/transl_table=11
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                   evidence=not_experimental
trans1 table=11
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complement (2924. .3910)
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predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                complement (2924. .3910)
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/gene="RSc0387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                            gene="ftsY"
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TITLE

codon_start=1

2842

2782

626

999

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The moore significant matches with motife in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest socring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, etg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most unstrain codon). If this cannot be identified we choose the most the most apparement initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (493. .1452)
//gene="SCSF8".02c"
//note="SCSF8".02c"
//note="SCSF8".02c, possible threonine dehydratase, len: 319
aa. Similar to many including: Bacherichia coli
SW:THD2 ECOLI (EWBL:M31312) threonine dehydratase catabolic
(EC 4.2.1.16) TdcB (3129 aa), fasta scores opt: 609
z-score: 676.6 E(): 3.2e-30 39.4% identity in 312 aa
overlap. Contains a Prosite hit to Serine/threonine
dehydratases pyridoxal-phosphate attachment site and a
pyridoxal-phosphate dependent artachment site and a
pyridoxal-phosphate dependent artachment.
                                                                                                                                                                                                                                                                                                           Submitted (05-JUN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Index Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H; UK On May 9, 2002 this sequence version replaced gi:8347023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 5F8 lies on genomic restriction fragment AseI-A bordered by cosmids 5H1 and 4G10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2. .109)
/note="nominal overlap with cosmid SC5H1 between bases
                                                                                                                                                                                                                                                 Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coelicolor A3(2)"
   Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor sequencing by the BBSRC and Beowulf Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .33285
/organism="Streptomyces
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complement (493. .1452)
/gene="SC5F8.02c"
/note="SC07292"
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                                                                                                                                          and Harris, D.
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                                                                                                                                                                                                            (bases 1 to 33285)
                                                                                                             (bases 1 to 33285)
                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                          Seeger, K.J.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                MEDLINE
PUBMED
                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGRTVARFTPARPGRETVLLLVEFYRRGEGWKVRALGQGYADGLAGLARDFGVETDD
APPEPATAPEPLTPGADSDGFLNLVNSARAAAGSPAVRPDPRLRSAARAHAAAMAAAG
TLSIETRDGVSVHQRVVSAGFAYLTVGEHLVSGPRTPAEFVAYCLRAERTRRTLHDTA
                                                                                                                                                                                                                 AEDASDLTDVLVSIGGGGLIAGVAAALRALRPGVRVWGVETEGAEAMSRALAAGGPLT
VPLSSVVTTLSAPSVSRLTYDHVAELVTEVLVVPDREAVRGSLALAEHAKVWTEPAAG
CLLPAARRVVERVGDGARIGLVVCGGNATVGDMAVWADRFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fasta scores opt: 467 z-score: 555.6 E(): 1.8e-23 36.6$ defatity in 205 as overlap and Streptomyces coeliscolor TR:CAB70638 (EMBL:AL137242) SCBF4.12C (239 as), fasta scores opt: 397 z-score: 474.2 E(): 6.1e-19 36.1$ identity in 183 as overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTVNGRNVLCFDASLSYRIATVKGSGIÄGGGLFNSVFTGQGRLGLVCEGNPLVIPVSQ
QYPVHVDTDAVVGWSAGLATSLHRSQSIGSMLRGGSGEAVQLVLQGEGFVVVRPSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTHAGWACVTGGPSGDTYWTALWAVPLTPDGLARTTAEVVGLTNRERAGAGLPALAVD
                                                                                                                                                    QRTGSFKARGATAKLLSLTEAERAAGVVAVSGGNHGIAVAVMAAALDVKATVVMPRTA
PARSVEIAEEAGALVRLTDGMDSAFALVTRLREEGLTLVHPFDDPVVVAGQGTVGLEF
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                                                                                                                          translation="MIAITEIEAAAERIAGHVVRTPTVPSPGLSALLGVPVTAKLELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCI7.21 (399 aa), fasta scores opt: 428 z-score: 449.2 E(): 1.5e-17 38.3% identity in 209 aa overlap" /codon start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SCSF8.04c, hypothetical protein, len: 434 aa.
Similar to Streptomyces coelicolor TR:Q9X9W9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCSF8.03c"
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                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry PF00291 S_T dehydratase,
Pyridoxal-phosphate dependent enzyme, score 210.10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similar to several proteins of undefined function
including: Deinococcus radiodurans TR:09RWP1
(EMBL:AE001920) conserved hypothetical protein (25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00165 Serine/threonine dehydratases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2167. .3471)
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complement (2167. .3471)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1288. .1329)
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                                                                                                                                                                                                                                                                                                        complement (547. .1413)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      E-value 3.3e-59'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SC07293"
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Warrener, P.,

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Stover, C.K., Pham, X.Q., Brwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, B., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.

Complete, genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MRLOVKGLQEKLGSQERQQADVSNQFGGGGKRLDGLASDLKAQQ
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KGTQDDLLVLKSQLDNFPAQGGNTAEPDAFRTQVMRNINTLQAQVQNLQQQLNTR"
complement (1529. . 2518)
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KVRRLVHLSSPSIYPDGRDHLDLNEEYVPRRFSDHYGATKYQAEQLVLSARDLGLEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALRPRFVVGAGDTSI FPRMI QAHRKGRLRI LGNGLNRVDFTSVHNLNDALFSCLLAGE
PALGKVYNI SNGQPVPFWDAVNYVMRQLDLPPVGGHLPYAVGYGLAALNBGVCRI LPG
RPEPVLFRLGMAVMAKNFTLDI NRAREYLDYDPRVSLWTALDEFCAWWRAQGL"
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RLRTWVWGGARNARGERRTARLETANVYDLTLHGVLLAVRHLLDYQGPGGYFTPSRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MRILVTGATGFIGGRFARFALEQGLSVRVSGRRADAVEHLVARG/
                                                                                                                                                                                                                                                                                                           Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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    10542
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                                                                                                                                                                                         opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="PA4361"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="PAO1"
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/transl_table=
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                                                                                                                                                            TITLE
                      aa. Similar to several other putative regulators from Streptomyces coelicolor including: TR:09XAN4 (EMBL:AL079355) SC4G6.06 (693 aa), fasta scores opt: 305 z-score: 328.7 E(): 7.7e-11 26.4% identity in 910 aa overlap and TR:092573 (EMBL:AL035569) SC8D9.18 (1091 aa), fasta scores opt: 857 z-score: 926.1 E(): 0 36.5% identity in 1077 aa overlap. Contains a Prosite hit to PS00017 ATP/GTP-binding site motif A (P-loop) Pfam match to entry PR0196 GerE, Bacterial regulatory proteins, luxR family. "/transI_table=11
possible LuxR-family regulator, len: 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLRFLLGRGVLQRPAGGAPGHRLALFASYRADDLHRRHPLRPLTAELVRLPGVERLE
LRFLEPDSDVRLVRLLRERRLEPSSTYRR I VERABGNAFYAELVAATDAFAGGVPSGL
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VSGDGGAYSFRHALAREAVYADLLPGERARLHGAFARLLAGPDRRSDSAAERAHTYRE
SHDLPEALAASLEAADHAQRVGAPAEELRHVEAALDLWTAVDAAARFAGPDAVTLTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEALGLI PAEPPSSTWVWAAATHVTAARQVGENETALRVARRALRAAEELAVTDARAD
LLISLISLEGGNRSTPEGRERLLEARELARRAGNAPVELRALFNLAIGCPESGDLEEC
LPWASEGLDRARRSGLLSSPYPREMRYLRLLVQYTLGHWDEVLRESAEHAGERSAVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HALGPGLIYVALARGDSGVADRARALLNGPFDWARMYAGVVLTDAAALRGDAEDAVRW
MRSSVETLTEAGTRPTVTLRLATLALSAVADTVTELRRAGDDAGVARWSDTAAELLAD
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Pseudomonas aeruginosa PA01, section 413 of 529 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAVLTAREQDVLRLLALGHSNRRIGEELFISAKTASVHVSNILAKLNAASRTEAVA
VAHRQGLVAPEPTSSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCRLRLADALLAADRREEAATEAGGVRREADRLGATVLRERVDDLVRRGRLAGPARAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18542 GGCCGTGCTCACCTGCCTGCCTGACCTCAACCCGCACGTCTACCTCGACACGT 18601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18659 cédadececcédecedecidericiderredecececeredecricodececececane 18718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18719 CGCCGCTTCCTGTCCCGCCCCTCGCCTGGCGGGTCCTCGACGGACTGGTGGCCGCCAC 18778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 TGTGTTTATCGGCGCGTCGGCGCGCAATACGGCGACACCGGACGGGGATTTTCGCCGC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGTT 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 GTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 GCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGTT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.6; DB 1; Length 33285; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 114; Indels
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/note="SC5F8.05c,
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AE004852.1 GI:9950587
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/translation="MSLTAIAFWVVLLLLAGYAVVLYNGLVRLKHAVGKAWANIDVLL
KCKHDELPKLVEACKGYMGHERATLERVIAARNAVASARERADVNALGKAESGLRAGG
GQLFALAENYPQLKANESFOPLSQLISGLENGIADRRELYNEAVNLNNVRIEGFPDLL
IARVAGEKAAELLOFSEAEKRADVDLKALFG"
                                                                                                                                                                                                                                                                                                                                                                                                            AAQGFVELYGVLEEGPEGPLQAPLTGKPCLWWRYRIEVEEKRSGREKAWRTVDKGASE
SPFSLRDATDACLVDPRGAEVRPLTQQRWEAFREAPIDTLRLLESFGTLVGGERLYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEERLIHAGEPLYALGEFRSSGGGRQGLDAERAQGAVIREWKGDFHGLLARFDSDGNGE
LDEREWNRVRLAARLEAEDRHRASSAAPTRHRLGKPGEAHPFILSSQGEDDLAVQLRR
QAAGAALLCLGSALLAGWLFSRLF"
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                                                                                                                                                                                                                                                                                                                                                                          translation="MDFDLRWLFIAASLGLCAWAGWQFVHRLARARLLGDVPTSRIRS"
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1 (Dases 1 to 24336)

McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.
Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559
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9
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Pred. No. 4e-05;
0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transI_table=11
product="hypothetical protein"
/protein id="AAG07757.1"
/db xref="G1:9950597"
                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="AAG07756.1"
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/gene="PA4369"
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/gene="PA4369"
                                                                                                          .9842)
                                                                                                                                                                                                                                                                                                                                \db xref="GI:9950596
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                                                                                                          complement (8940.
/gene="PA4368"
                                                                                                                                                                                   /codon_start=1
/transl_table=11
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AE008841.1 GI:16421612
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/transl_table=
                                                                        gene="PA4368"
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Similarity 55.0%;
49; Conservative (
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Matches 149;
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AE008841/c
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                                                                                                                                                                                                                                                                                      RVGQPVLVRETPPHPTDLGRRILLINHVQQVRLLEGDLQRWVPNIDEGGAPERLRIAIANA DSLATWWAAAVGDFCAERRVLLDLVVBDQEVGLKRMRAGEVAGCVCGSARPVAGARSL
LLGAMRYRGLASPDFIARHFPRGVEAAALAGVPAIVFGPDDLLQHRFLKDLGVEGGFI
HHLCPSSEGFVRLTAGGLGWGLVPERQVQGELARGELVELLFGQVIDVPLYWHNG
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KWYTTANDILASIESNSHLRREAENDILRISQYDFITGLPRRQLLQQQLDQILDGAG
RQQRRVAVLCLGLDDFWGINRQYTYGLOGDQLIJALADBIRGHGARLGSARLGSDQFA
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6876. .8939

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/codon start=1

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                                                                                                                                                                                                                                                                                                                                                                                                                                               GELLASLTEHLLARAGDGLVRVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAG07752.1"
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'transī table=
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SGS

CDS

CDS

Du, F.,

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/RC number="5.3.1.6"
/nofe="similar to B. coli ribosephosphate isomerase,
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aa), 98% identity in aa 1 - 219"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3281. .3286)
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/gene="iciA"
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Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such ass compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.rigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to E. coli putative ligase (AAC75949.1);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/and Pedro Romero and Peter Karp at EcoCyc;
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="ygfA"
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                                                                                                                                                                                                                                                                                 2 (bases 1 to 24336)
The Salmonella typhimurium Genome Sequencing Project.
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                                                                                                                                                                       Nature 413 (6858), 852-856 (2001)
21534948
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/gene="ygfA"
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.33. .2277
'gene="sbm"
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                      SOURCE
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/db_xref="GI:16421618"
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VMKQRWKIATAMLATWLNHYYYLLDTFVVLGSLGGQLAMEPKRWFALGTISASFLWF
FGLALLAAWLAPRLRTAKAQRIINILVGVVMWLIAFQLAREGVAHMHALFN"
complement (6067. 6072)
                /tränglation="MKPKVMALAALVGLSAMSAQASELPEGPHIVTSGTASVDAVPDI
ATLAIEVNVAAXDAATAKKQADERVAQYLSFLEQNQIAKKDISAANLRTQPDYDYQNG
KSILKGYRAVRTVEVTLRQLDKLNSLLDGALKAGLNEIRSVSLGVAQPDAYKDKARKA
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                                                                           AIDDAIHQAQALAAGFNSKLGPVXSVRYHVSNYQPSPVVRMMKAADĀAPVSAQETYEQ
PTIQFDDQVDVVFQLEPGTGQTSTTAASTQ"
complement(5336. .5341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="incolved in stability of MscS mechanosensitive channel; similar to E. coli putative transport protein (AAC75961.1); Blaetp hit to AAC75961.1 (286 aa), 91% identity in aa 1 - 285" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5983 idaigaarcaggaarrcgrcgccagraccacrcargaragcgcrrrgcgcgrraa 5924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5863 cerecerecresereareareasesesesesereserrerrerrariseraceserrire 5804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /wore="putative RBS for yggA; RegulonDB:STMS1H003109"
complement(6259, .7131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTGTTTAATTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 CTGACGICTITITIGITCATCGCCGGCACCTTGGGCGTTGATCTTTTGTCCAATGCCGCGC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGATCGTGCTCGATATTATGCGCTGGGTGGCATCGCTTACCTGTTATGGTTTGCCGTCA 262
                                                                                                                                   ...o.e="putative RBS for yggE; RegulonDB:STMS1H003108"
complement (5424. .6072)
/qene="www.res"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                             note="similar to E. coli orf, hypothetical protein AAC75960.1; Blastp hit to AAC75960.1 (211 aa), 90% dentity in aa 1 - 211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 TTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTACTGG 82
                                                                                                                                                                                                                                                                                                                                                          'transT_table=11
'product="putative LYSE family amino acid transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5923 GTGATTTAGTCCTGATTAGCGCCGGTATTTTTGGCGCGTAGCGCGTTGCTGATGCAGTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5803 GCGCCTGAAACGGCAATGAGCAGTAATCTGGA 5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 TGGCAGCGAAAGACGCCATGACAAACAAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (6259. .7119)
/gene="ygg8"
                                                                                                                                                                                                                                       complement (5424. .6059)
xref="GI:16421617"
                                                                                                                                                                                                                  note="STM3066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="STM3067"
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                                                                                                                                                                                                                                                              gene="yggA"
                                                                                                                                                                                                      gene="yggA"
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AE005522/c
LOCUS
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linear BCT 21-MAR-2001 contig 3 of 3, section 141

DNA genome,

AE005522 10701 bp Escherichia coli 0157:H7 EDL933 0f 290. AE005522 AE005174 AE005522.1 GI:12517448

> DEFINITION ACCESSION VERSION

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Strain
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QHURNLLAAAVNAARVRATLGEISDALEAAFDRYLVPSQCYTGVIAQSYHQSEKSASE
FDAIVAQTEQPLADNGRRPRILIAKMGAGLDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
EETARLAVENDVHVVGASSLAAGHKTLIPELVPRALKKWGREDICVVAGGVIPPQDYAF
LQERCVAAIYGPGTPMLDSVRDVLALISQHD"
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NURTYGTLPGLPPYVRGPRATWYTRQPWTIRQYAGFSTARENAFKSNAFKNIAAGQKGL
SVAPDLATHRGYDSNPRVAGDVGKTGVAIDTVEDMKVLFDQIPLDRGSVSWFMKGAV
LPVLAFYIIAABEQGVTPDKLIGTIQNDILKEYLCRNTYIYPPRESMRIIADIIAWCS
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IRTTIEALAATLGGTQSLHTNAFDEALGLPTDFSARIARNTQIIIQESSELCRTVDPL
AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 714 are 99.15 pct identical from Escherichia coli K-12 Stra
                               Bscherichia coli O157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Pernah. NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Maybew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
Grocbeck, R.J., Davis, N.W., Lim, A., Dimalanta, B., Potamousis, K.,
Apodaca, J., Ananthazaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A., and Blattner, P.R.
                                                                                                                         1 (Dases I to 10701)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grobeck, B.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                        Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
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Submitted (22-OCT-2000) Laboratory of Genetics, University
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transT_table=11
/product="putative nucleotide-binding protein"

    10701
/organism="Escherichia coli O157:H7 EDL933"

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//note="Residues 1 to 331 of 331 are 99.69
residues 1 to 331 of 331 from Escherichia
MG1655: B2918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product==methylmalonyl-CoA mutase (MCM)"
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/db_xref="taxon:155864"
Escherichia coli 0157:H7 EDL933
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/gene="sbm"
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/gene="ygfD"
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/gene="ygfD"
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gene

CDS

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/codon start=1
/transI_table=11
/product="putative actin"
/product="putative actin"
/protein id=#Ad5sB48.1"
/db_xref="GI:12517454"
/translation="MKFKVIALAAMGISGWAAQANELPDGPHIVTSGTASVDAVPDI
ATLAIENWAAKDAPATAKKQADERVAQYISPLELNOIAKKDISSANIRTQPDYDYQDG
ATLAIENWYARTWYTLEQUDKLASLLIDGALKAGINEIRSVSIGVAQPDAYKDKAA
AIDNAIHQAQELANGFHRKLGPVYSVRYHVSNYQPSPMVRMMKADAAPVSAQETYEQA
AIQPDQVDVVPQLEPVDQQPAKTPAAQ"
complement (7456. 8091)
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isdlylichgirgssallwospwilalvrwggvvrflwygrgarxramssnielashe
VLKggrwri iarmlavrwinbhyvldfrvvlgslggoldvxpkrwpalgtisasflwr
FGIAllaaMilapkirzaksoriinLvvgcvwwFlalollarbgiaHaQalfs"
complement (8230. .9090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="orf; Unknown function"
/note="Residues 1 to 211 of 211 are 98.10 pct identical to
residues 1 to 211 of 211 from Escherichia coli K-12 Strain
MG1655: B2923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / FTATALIONE "MEDLAVVDSINGAGSWLVANQALLLSYAVNIVAALAIIIVGLII
ARMISNAVNRLMISRKIDATVADFLSALVRYGIIAFTLIAALGRVGVQTASVIAVLGA
AGLAVGLALQGSLSNLAAGVLLVMFRPFRAGEYVDLGGGVAGTVLSVQIFSTTWRTADG
/function="phenotype; Not classified"
/note="Residues 1 to 246 of 246 are 100.00 pct identical
to residues 1 to 246 of 246 from Escherichia coli K-12
Strain MG1655: B2922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="putative transport; Not classified" // foote="Residues 1 to 286 of 286 are 100.00 pct identical to residues 1 to 286 of 286 from Escherichia coli K-12 strain MG1655: B2924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTTTCAAGGTCTTGCTCTTGGGGCAGCTATGATTCTGCCGCTCGGCCCAAAATGCT 8020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAGCGATTTGGTCCTGATTTGCGCGGGATTTTTGGTGGTGCGCGTTATTGATGCAG 7900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7899 redecetrecreseres recenseres de 1840 redecensor recensor recensor reservados de 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATTACAGGTCTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8019 TTTGTGATGAATCAGGGCATTCGTCGTAGTACCACATTATGATTGCCTTACTTTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTICIGACGICITITIGITCATCGCCGGCACCTIGGGCGTIGATCTTTTGTCCAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1; Length 107
Pred. No. 9.1e-05;
0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transI_table=11
/product="putative transport protein"
/protein id="AAG58050.1"
/db_xref="GI:12517456"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon start=1
/transI_table=11
/product="corf, hypothetical protein"
/protein id="AAG58049.1"
/db_xref="GI:12517455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITGGCGCTTTTAAAACAGCGAIGAGTAGTAATATIGA 7802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCATGGCAGCGAAAGACGCCATGACAAACAAGGTGGA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7456. .8091)
/gene="yggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8230. .9090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Z4260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Z4261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="yggB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.78:
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Conservative
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Matches 143;
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                                                                                                                                                             GDKTRUNDLARAEAAFIRPVESGHLGGASGRARELMLLCRAAGYDVJVETVGGG
ETBVARMVDCFISLQIAGGGDDLQGIKKGLMEVADLIVINKDDGDNHTNVAJARHMYE
SALHILRRKYDEWQPRVLTCSALEKRGIDEIWHAIIDFKTALTASGRLQQVRQQGSVE
WLRKQTEEBYLNHLFANEDFDRYYRQTLLAVKNNTLSPRTGLRQLSFFIGTGYFD"
                                          /db_xref="GI:12517450"
/translation="MINEATLAESIRRLRQGEHATLAQAMTLVESRHPRHQALSTQLL
DAIMPYCGNTLRLGVTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQI
TRMIQKFPRVIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSWTPVNLGVPYNLVGIH
NLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPL
AIAVIKEELRVLGEAHTWNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="putative enzyme; Not classified"
/note="Residues 1 to 492 of 492 are 99.39 pct identical to
residues 1 to 492 of 492 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWIJTSGIGNAPTWILRAKKVIIE
LHYHDPRVABELADIVIPARAPRRAVSIFHAMSVGTRYVOIDPKKVYAVYTSLID
AGNMLDKQNPAGLADIVYTPLLQENAHGRIPPELPLQSGYGNINNAVMARLGEND
EIPPFWMYSEVLQESVVHLLETGKISGASASSLITSADSLRKIYDNMDYFASRIVEND
EISPPFWMYSEVLQESVVHLLETGKISGASASSLITSADSLRKIYDNMDYFASRIVURD
EISNPREIIRRLGVIALUNGLBEDIYGHANGTHAMOTHQEDIANGGSGDFERNAYLSI
FWARSINGTAKEGKISTYVPMCSHVDHNEHSVKVIITTEQGIADLRGLSGLSPERNAYLSI
FWARSILTENGARAFIJHDLSHVFDLHNNLIATGSMLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="METQWTRWTADEAAEIIQHNDMVAPSGFTPAGSPKALPTAIARR
ANEQHEAKKPYQIRLLIGASISAAADDVLSDADAVSWRAPYQTSSGLRKKINQGAVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative regulator; Not classified" hote="mesidues 1 to 192 of 192 are 99.47 pct identical to residues 6 to 197 of 303 from Bscherichia coli K-12 Strain MG1655: B2921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OIGYTLFTRKDNNISLNKAGGELYQKLFPVYQRLSAIDNEIHNSGRRSREIVIGIDNT
YPIIIFDQLISLGDKYEGVTAQPVEFSENGVIDNLFDRQLDFIISPQHVSARVQELEN
LTISELPPLRLNFLVSRRYEERQEQELLQELP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MDIFISKKMRNFILLAQTNNIARAAEKIHMTASPFGKSIAALEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tunction="putative enzyme; Not classified" /note="Residues 1 to 275 of 275 are 100.00 pct identical to residues 1 to 275 of 275 from Escherichia coli K-12 Strain MG1655: B2919"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon start=1
/transl_table=11
/product="partial putative transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product = "putative coenzyme A transferase" | protein id="AAGS8046.1" 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="AAG58047.1"
db_xref="G1:12517453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative enzyr/
/protein id="AAG58045.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5878. .6456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ygg&"
/note="24259"
complement(6623. ,7363)
/gene="ygg&"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6623. .7363)
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                                                                                                                                                                                                                                                                                                                                    3234. .4061
/gene="ygfG"
/note="Z4256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Z4257"
4085. .5563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4085. .5563
/gene="ygfH"
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/gene="ygfH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3234. .4061
/gene="ygfG"
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                                                                                                                                                                                                                                                                                               Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and Shinagawa, H.

Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the encerohemorrhagic Escherichia coli 0157:H7 Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrying the
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Submitted (26-UNN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail: Ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                            BCT 07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                          Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
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Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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Shiga toxin 1 genes of the enterchemorrhagic Escherichia coli
0157:H7 strain derived from the Sakai outbreak
Gene 258 (1-2), 127-139 (2000)
                                         PO02563 266658 bp DNA linear BCT 07-MJ scherichia coli O157:H7 DNA, complete genome, section 14/20
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1. .266658
/organism="Escherichia coli O157:H7"
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/sub_strain="RIMD 0509952"
/db_xref="taxon:83334"
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/gene="EC83650"
complement (244. .693)
/gene="EC83650"
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AP002563.1 GI:13363121
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/product="hypothetical protein"
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/translation="hybrid" protein id="c
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MEPLEWLQWVLIPRMHDLLANNQPLPGAFAVAPYYEMALATDHPQRALILAELEKLDA
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TWSEDDFRRVQENLIGHLVTQKRLKLPPTLFIATLEEELEVISVCNLSGEVCKETLGT
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PLVEELDKIADKFAREDKGPOPAVTHYRGLATVEMPVATGRYPTTRYGLVELEPKTGR
KHOLRRHLAHLRHPIIGDSKHGDLRONRSGAEHFGLORLMLHASQLSLTHPFTGEPLT
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100 in 149 aa (Conserved in E.coli K-12)"
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Appene="RESASS2"

/note="similar to B2792_ECOLI gi|1789156 percent identity

98 in 109 aa (Conserved in E.coli K-12)"
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/gene="EC83651"
/fore="similar to YQCB ECOLI gi|1789155 percent identity 99 in 260 aa (Conserved in E.coli K-12)"
/codon_start=1
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/db_xref="G1:13363123"
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protein id="BAB37075.1"
/db xref="G1:13363124"
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/evidence=not_experimental
/transl_table=11
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/transl_table=11
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/transl_table=11
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/gene="csrB"
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/gene="ECs3653"
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/gene="EC83653"
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/gene="ECs3654"
3057. .3905
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Abromonas salmonicida oriC replication inhibitor (iciA), N-acyl homoserine lactone synthase (asal), transcriptional activator (asaR) and Ygga (ygga) genes, complete cds, and 2'3'-cyclic phosphodiesterase (cdpB) gene, partial cds.
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OPAEPLLIRSOPLOATPLGOKLLAHYRQVRQLELELAGEIAPDEPOAPIRVSIAVNAD
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LGEMYYLTASAPAVARHFPAGLTPAALAKTPAVAFDQRDDMHVSFWARHFGLEPGGY
PCHTVRSSEAFVANARDGLAYCLIPELQIRQQLAGGILLDLSPSHHLIEPLYWHRWVL
ERGLHKQISORLISEGRRALOPG"
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DSFDTPDTHWVLIEDEEGLCGCIRLLSCAQDYMLPSIFPTALAGEAPPRSSDVWELTR
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Swift,S., Karlyshev,A.V., Fish,L., Durant,E.L., Winson,M.K., Chhabra,S.R., Williams,P., Macintyre,S. and Stewart,G.S. Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate N-acylhomoserine lactone signal molecules J. Bacteriol. 179 (17), 5271-5281 (1997)
                                                                                                           Db 161401 rédecérregridéredecriserentérédecedeceradrerretrecriserenter 161342
Db 161461 ATCAGCGATTTGGTCCTGATTTGCGCGGGATTTTTGGTGGTGCTAGCGCGTTATTGATGCAG 161402
                                                               258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4033)
Swift, S., Karlyshev, A.V., Fish, L., Durant, E.L., Winson, M.K.,
williams, P., MacIntyre, S. and Stewart, G.S.A.B.
Direct Submission
                                                         199 GCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="TciA; similar to Escherichia coli IciA"

/codon start=1

/transl_table=11
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/product="N-acyl homoserine lactone synthase"
/protein_id="AAB70017.1"
/db_xref="GI:1519236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="oriC replication inhibitor"
/protein_id="AAB70016.1"
/db_xref="GI:1519235"
                                                                                                                                                                                                                      Db 161341 Trrggcgcrrrrraaacagcgargagragraarrga 161304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Aeromonas salmonicida"
/strain="NCIMB 1102"
                                                                                                                                                                    GTCATGGCAGCGAAAGACGCCATGACAACAAGGTGGA 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:645"
complement(30..929)
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                                                                                                                            KADNI-PROGTDIWTLYELSWINAKGI-POVAVHYELDYTSVNI-IESKSFKLYLNSFNO
TRFNNWDEVROTLERDLSTCAQGEVSVALYRLDELEGQPIGHFNGTCIDDQDITIDNY
BFTTDYLENATSGEKVVEETLVSHLLKSNCLITHQPDWGSIQIQYRGRQIDREKLLRY
LVSFRHHNEFHEQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRSNSDFVPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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/db_xxef="G1:13863127"
/db_xxef="G1:13863127"
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GSLTDNSKELLSRERFDINVLRERGYMLBLINPPERAFVDGRIIRALQANLFAVLR
DILFYYGQIHNTVRFPNLMLDNSVHITMLVFSILRNARALHYGEAPNMVVCWGGHSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENEYLYARRVGNOLGLRELNI CTGCGPGAMEAPMKGAAVGHAQORYKDSRFIGMTEPS
IIAAEPPNPLVNELI IMPDIEKRLEAFVRIAHGIII PPGGVGTAEELLYLLGILMNPA
NYDQVLPLILTGPKESADYFRVLDEFVVHTLGENARRHYRIIIDDAAEVARQMKKSMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="METTOTSTIASKDSRSAWRKTDTWWMLGLYGTALGAGYLFLPIN
AGYGGMIPLIIMAILAFPWTFFAHRGLTRFYLSGKNPGEDITEVYBEHFGIGAGKLIT
LLYFFAIYPILLVYSVAITNTVESFMSHQLGMTPPPRAILSLILIVGMMTIVRFGEQM
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SLAGAAKEQNISILSYLANHFNAPVIAMMAPIIAIIAITKSFLGHYLGAREGFNGMVIK
SLRGKGKSIEINKLNRITALFMLVTTWIVATLAPSILGMIETLGGPIIAMILFLMPMY
SLRGVPAMRKYSGHISNVFVVVMGLIAISAIFYSLFS"
1285. .8652
                                                                                                           translation="MSSYANHQALAGLTLGKSTDYRDTYDASLLQGVPRSLNRDPLGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVKENRRDTGDAYSFNWSNRIAPDLQMPFEPSHENMANLKLYPDQPVEVLAÄDLRRAF
SGIVAGNVKEVGIRAIEEFGPYKINGDKEIMRRMDDLLQGFVAQHRNKLPGSSAYIPCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="similar to SDAC_ECOLI gi|1789160 percent identity
100 in 429 aa (Conserved in B.coli K-12)"
//codon_start=1
//evidence=not_experimental
//trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SDAA ECOLI gi|1788116 percent identity 77 in 455 aa, similar to SDAB ECOLI gi|1789161 percent identity 99 in 455 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                     note="similar to YGDH ECOLI gi | 1789159 percent identity in 454 aa (Conserved in E.coli K-12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="probable serine transporter"
protein id="BAB37075.1"
db_xref="GI:13363128"
                       /product="hypothetical protein"
/protein_id="BAB3707%,1"
/db_xref="G1:13363126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 1; I Pred. No. 0.00014;
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/evidence=not_experimental
/trans1_table=11
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5938. .7227
                                                                                                                                                                                                                                                                             017. .5381
gene="ECs3655"
                                                                                                                                                                                                                                                                                                                                   1017. .5381
/gene="EC83655"
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gene="EC83656"
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Best Local $
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Job time : 2268.29 secs

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/trānslation="MKLGAIAAIVLLSACSNENDSKTQPGAVALRLIQTSDIHSNVLG
YYYQNKENBKFGLSRTALLIRAARSENPNNLLLDNGDLLQGTPLADYIFEQSGAGYL
DKQAHPVFKAMNELGYDAGNGNHEFNYGLDYLTKTLQ"
1160 c 1229 g 857 t
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LAI DANRAPRMGNGVSELTCVI FREVYAFARAKGI RELVAVVSLPVERI FRRLGLPI E
RLGHRQAVDLGAVRGVGI RFHLJERFARAVGHPMQGEYADARELVTE"
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MSMQRPKVVLENQCPDSWVQAYTANHMLACDPIIQLARKQTLETYWRRLDERARFLQ
GSLDVWGLAAEFGLRNGISFPLHGAAGENGILSFTTAERASSDLLLESSPILSWMSN
'IFEAIRIYRVSLEEDDPQEALTDRETECLFWASEGKTSGEIACILGITERTVNYHL
KQYTRKTGSWNRYQAIAKGVSGILLPNLEQVVVTNFPKLMQ"
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\text{CranslabstrimgGYTLFLCWFGTRSLRSBAWQGQAALADSPRLMGYKSYLAMTL
\text{NYTLARHYYLDTIMLGSFGSQPAEPLRPAFAAGAMLASLWFYSLAFGAALSPWL
\text{ARRYQQAIDTIVGLIMLGILALQLASGALLAS"}
\text{ARRYQQAIDTIVGLIMLGILALQLASGALLAS"}
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- Web: www.genoscope.cns.ft)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digetion of Drosophila DNA provided by the BDGP from the isogenic strain vised for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex – FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                          TGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTGTTTAATTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTTGATCTTTTGTCCAATGCCGCGC 202
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                                                                                                                                                      1; Mismatches 137;
                    1. 830
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="22224"
/clone lib="NotreDamel"
/note="end:T7"
/ a 231 c 227 g 156 t
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Location/Qualifiers
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mays cDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
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/dev_stage="just after the transition from vegetative to
inflorescence development"
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/clone_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                  571 SCSCCSSCSCSSSCSCCCCCCCCCSCSSSSSSKCSSTSBSCSCCCSSKSVCGTS 630
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Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                   511 others
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
TTE: 650 723 227
Fax: 650 725 8221
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/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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/cultivar="OH43"
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Gaps

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Length Indels

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United (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - The BDP is constructing a physical map of the Drosophia Genome Project (BDGP). The BDCP is constructing a physical map of the Drosophia melanogaster genome using these BAGe. For futher information please see http://www.fruifily.org The BDGP Drosophia melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digestion of Drosophia DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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                                  /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutacor plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Matches 149; Conservative
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                        /note="Organ: tassels; Vector: HybriZAP; Site 1: EccRI; Site 2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 CTCTCGTAGTAGACGAGGTGGGAGCGAAGTGGACGTAGCAGGTGCCGGCGAGGTGGATC 245
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/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAGCAGCAGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAAC 468
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                                                                                                                                                                                                                                                                                                                                                                                                                          349 TTGGGCGGTTCGGCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTC 408
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/dev_stage="fully-grown"
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                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                          Score 44.4; DB 14;
Pred. No. 0.033;
0; Mismatches 176;
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855 California Ave, Palo Alto, CA 94
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945001 row: E column: 08.
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/lab host="XLOLR"
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648

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/note="Vector: Lambda Uni-ZAP XR, excised phagemid, site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give palluescript the University of California, Riverside. Plasmid DNA the University of California, Riverside.
                                                      /clone_lib="Wheat pre-anthesis spike cDNA library"
filssue_type="Spike before anthesis"
/dev stage="Adult plant"
/lab_host="E. coli SOLR"
                  /db_xref="taxon:4565"
/clone="WHE0967_G03_M05"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE498441 613 bp mRNA linear EST 04-AUG-2000 WHE0967_G03_M05ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0967_G03_M05, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, O.D., Chao, S., Choi, D.M., Close, T.J., Fenton, R.D., Han, P.S., Haia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGACC--TGGTTGAACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGGCGTC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSSTSSCTSTKGYSTSTBSYSBTTBTBTTSTSTBBTTBTTSTBTTBTTSTTAMTST 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGC 630
                                                                                                                                                                                                                                                                                                                        GGTGGAGGTGAGCGTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGT 452
                                                                                                                                                                                                                                                                                                                                                                                                       578 SSCGCGSCSYSSSTGSTGSCGCGSSSSSSSSSSSSTSTSTSSSTSGCGYSSSGSBSSC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 GCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGCGCAACCGGGTGCG 392
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http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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                                                                                                                                                                                                                    Length 910;
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                                                          melanogaster"
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US Department of Agriculture, Agriculture Re
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                    5.8%; Score 41.2; DB 17;
14.8%; Pred. No. 0.35;
                                                                                                                                                                                                                                                           Conservative 150; Mismatches 119;
                                                                                                                                                            198 t
                                                      /organism="Drosophila mw./db_xref="taxon:7227"
/clone="BACR14721"
/clone_lib="RRCI-98"
/note="end : T7"
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Web: www.genoscope.cns.france le-wail: Sequelegenoscope.cns.fr

Web: www.genoscope.cns.france le-wail: Sequelegenoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Gooegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain v2: on bw sp, the same strain used for the BDGP's

Pl and BST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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preparations and DNA equencing were performed in the OD Anderson lab (all other authors)."

178 c 188 g 102 t 1 others
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster
Bukaryota; Mecazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                  Length 613;
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                                                                                                                                                                                                                  Score 40.2; DB
Pred. No. 0.61;
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AL053013
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Best Local Similarity 53.5%;
Matches 84; Conservative (
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/organism="Triticum aestivum"

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HTC 25-MAY-2002
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
     /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Handety, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Overgo Probes
2 (bases 1 to 950)
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Submitted (25-APR-2002) Maize Mapping Project, University
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                                                                                                                                                                              Length 1667;
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Location/Qualifiers
1. 950
/organism="Zea mays"
/db xref="MaizebB:635429"
/db xref="taxon:4577"
/clone="PCO095355"
                                                                                                                                                                          5.6%; Score 39.6; ilarity 47.2%; Pred. No. 1.. Conservative 0; Mismatches
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Zea mays PC0095355 mRNA sequence.
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Best Local S
Matches 120
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(Dases 1 to 1667)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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/db_xref="MaizeDB:633502"
/db_xref="texcon:4577"
/clone="PCO065133"
/clone="pCO065133"
/clone="pCO065133"
/clone="lib="Maize Mapping Project/DuPont Cornsensus Library"
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Submitted (25-ARR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. .1667
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                         melanogaster"
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1. .925
/organism="Drosophila muda xref="taxon:7227"
/clone="BACR:9D16"
/clone lib="RPCI-98"
/note="med : TET3"
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Zea mays PC0065133 mRNA sequence
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Unpublished (2002)
2 (bases 1 to 1667)
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Matches 109; Conservative
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(bases 1 to 557)
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/clone lib="945 - Mixed adult tissues from Walbot lab,
same aB 707 (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tissue_type="tassel, kernal, silk, husk, root, leaf"
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                                                                                                                                                                                                                                                                                                                                                                                               409 GATAAGCAGCGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAAC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 CTCTCGTAGTAGACGAGGTGGGAGCCGAAGTGGACGTAGCAGGTGCTGCCGAGGTGGATC 273
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                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 ACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTG
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          11; Length 950;
                                                       Pred. No. 1.6;
0; Mismatches 185; Indels
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Location/Qualifiers
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/lab_host="DH108"
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     Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/cultivar="W23"
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Query Match
Best Local Similarity 46.5%;
Matches 166; Conservative
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AUTHORS
TITLE
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Ste_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
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Plate: LLAM10981 row: g column: 08
                                                                                                                                                                                                         331 TTGGCCTGGACGCCGGAGAGGTCCGAGATGGCGCCCCTGGAGAGCTTGCCGGTTATGGTC 272
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                    Gaps
                                                                                                                                                349 ITGGCCGGTCGCCGCGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGTC
                                                                                                                                                                                                                                                                     409 GATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAAC
                                                                                                                                                                                                                                                                                                                             271 CTCTCGTAGTAGACGAGGTGGGAGCCGAAGTGGACGTAGCAGGTGCTGGCGAGGTGGTC
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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla
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Pred. No. 3.2;
0; Mismatches 60; Indels
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 Tricicias de ceracitades cada recitrica cecesada 106
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/db_xref="taxon:10090"
/clone="IMAGB:4980895"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev stage="5 months"
/lab_host="DH108"
5.5%; Score 38.8; DB 10;
48.2%; Pred. No. 1.6;
tive 0; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 903)
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Best Local Similarity 55.2
Matches 74; Conservative
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/userisme="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="texon:4565"
/clone="whal2a03"
/clone="whal2a03"
/clone="whal2a03"
/clone="whal2a03"
/clone="whal2a03"
/clone="whal2a03"
/dev stage="seed DRA30"
/dev stage="Reekes" scale 11.3"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: Brookl; Site 2: XhOi; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled from the tissue, polyA was purified from the pooled from the tissue, polyA was purified from the pooled from the two samples, polyA was purified from the pooled from the tissue, cluster was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Chose, Fentom, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were performed in the Ob Anderson lab (all other authors)."
                                                                                                                                                                                                                                                           BJ295166 BJ295166 Y. Ogihara unpublished cDNA library, Wh_SL Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooideae
; Triticeae, Triticum.
I (bases 1 to 370)
Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 GGCGGAGGCGACCAAGGACACGGCTGGAAGGCGGCGGCCAAGGATAAGGCCAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 GGCGGCCAAGGACGCCACGTTGGAGAAGACGGCGTCGGCCAAGGACGCCCGCATGGGAGAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 ACCAACCGIGCCCGAIGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGCGCGAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 GGCAGCGAAAGACGCCATGACAACAAGTGGAAGCGCCACAGATCATTGAAGAAACAGA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 370;
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                                                   424 AATACCCTGGTCGGCCTGGTRATGTGGTTTATCGCTTTCCAGCTG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed genes in Triticum aestivum Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
              652 AACGICGICGIGGCAGIIGIGAIGACCGCAIIGGCCAICAAACIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        BJ295166.1 GI:20109847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bread wheat
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BJ295166/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae GSS SP6 end of clone 08N07 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito), 81144476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (16-PEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
           186
                                                                                                                                     TIGICCAAIGCCGCCCGAICGIGCICGAIAITAIGCGCIGGGGGGGCGICGCAICGCITACCIG 246
                                                                                                                                                                                                       500 igcricércecrédiéceceércériéreiriririéceardadirececedecreces 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Web : www.genoscope.cns.fr)
2 (bases 1 to 804)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AAGCAGCGGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 ArdaAgcaccacracaAdarraicaicaccaracracacadaicaidacraaacca 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1 (bases 1 to 804)
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This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Blochem. and Biol. Molec. of Insects, Institut
   CTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTTGATCTT
                                                                  560 cricircarcricia de contra 
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Pred. No. 3.6;
1; Mismatches 143;
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/note="end : SP6"
257 c 207 g 14
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/clone="08N07"
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Anopheles gambiae
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Best Local Similarity 48.1%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                  247 TTATGGTTTGCCGT 260
                                                                                                                                                                                                                                                                                                                              Genoscope
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VERSION
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CNS01HIJ/c
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Direct Submission

Submitted (06-58P-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces hluyverin, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                       CNS06D94 644 bp DNA linear GSS 17-JUN-2001
                                                                                                                                                                                                                                                                                                                                          Eukaryotan Fungi; Asconaronycetaceae; Eygosaccharonycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

1 (bases 1 to 644)

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Belotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Malpertuy, J., Dulon, B., Durrens, P., Lephingle, A., Librente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Porier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471 GAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGCGTCGGCGCGCAATACGGCGACAC 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 644)
Mincharigmy, J., Straub, M., Potier, S., Tekaia, F., Dujon, B.,
Wincker, P., Artiquenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 644;
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                                                                                                                                                           lygosaccharomyces rouxii, genomic survey sequence
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/strain="CBS 732"
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32.7%; Pred. No. 5;
iive 50; Mismatches 139;
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/clone="AR0AA011D12"
/clone_lib="AR0AA"
/note="end : T7"
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PBS Lett. 487 (1), 52-55 (2000)
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GSS.
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wes 92; Conserv
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                           RESULT 15
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                                                                                                                                                           BH843100 451 bp DNA linear GSS 13-JUN-2002
TC3-54P23.TV TC3 Trypanosoma cruzi genomic clone TC3-54P23, DNA
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma, Schizotrypanum.
1 (bases 1 to 451)
Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A., Munden, H.,
Nelson, S., Pentony, M., Rinta, J., Robertson, L., Seyler, A., Sisk, E.,
Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M., Ghedin, E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mylerpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Peter Myler
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .451
/organism="Trypanosoma cruzi"
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larity 50.0%; Pred. No. 4.4;
Conservative '0; Mismatches
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/db_xref="taxon:5693"
/clone="TC3-54P23"
/clone_lib="TC3"
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Fax: 206 284 0313
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Search completed: April 27, 2003, 00:51:19 Job time : 955.401 secs

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Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
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AAI99682
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02-JUL-1999;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
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22

4403765 636 15239

1568

Result Š. Seguence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;

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Claim 3; Page 233-234; 1737pp; English.
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99DE-1042076.
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09-MAR-2000;
                                                                                                                                                                           11-AUG-1999;
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                  Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases
Zelder O, Haberhauer G;
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WO200166573-A2

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methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
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                                 Gaps
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 Length 822;
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Query Match 100.0%; Score 711; DB 22; Best Local Similarity 100.0%; Pred. No. 2.8e-206; Matches 711; Conservative 0; Mismatches 0;
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This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, and an animal feed additive. Other (A) are varioualy useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Juncreasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium
    TTGGACGCGTTTGTGTTTTATCGCCGCGCGCGCGCATACGGCGACGCGACGGTGG
                                             541 ATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
                                                                       ATTITCGCCGCTGGCGCGTTCGCGGCCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC
                                                                                                                             GCAGCAGCATTGTCACGCCCCCTGTCCAGCCCCAAGGTGTGGCCGCTGGATCAACGTCGTC
                                                                                                                                                            GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
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                                                                                                                                                                                                              GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGTTAG
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/label= LysE
complement (1723..2373)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 23 and 26; Page -; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (82..954)
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/label= LysG
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/label= orf3
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P-PSDB; AAW37714-16.
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                                                                                                                                                                                        G, Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel Corynebacterium
                                                                                                                                                                                                                                                                                                         Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAV71922). The metabolic pathway proteins of the invention include enzymes involved in the lysing and methionine biosynthetic pathways. The polymucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria. AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention.
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                                                                                                                                                                                        Zelder O, Haberhauer
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                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 214-215; 316pp; English.
                                                                                                                                                                                      Schroeder H,
                                    22-DEC-2000; 2000WO-IB02035.
                                                                              09-MAR-2000; 2000US-187970P. 23-JUN-2000; 2000US-0606740.
                                                                                                                                                                                      B,
                                                                                                                                                                                    Kroeger
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                                                                                                                                                                                                                                                                    P-PSDB; AAU71888
                                                                                                                                                                                                         Hwang B;
                                                                                                                                          (BADI ) BASF AG.
13-SEP-2001
                                                                                                                                                                                 Pompejus M,
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                             Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 other;
                                               , DB 18;
4.5e-206;
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NB. This sequence has been created of the specification.
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from Coryneform bacterium. Coryneform bacterium acteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein
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Ozaki A;
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Pred. No. 4
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Senoh A, Ikeda M,
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16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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Tateishi N,
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                                Sequence 708 BP; 134 A; 173 C; 221 G; 180 T; 0 other;
                                                                                                                                                               1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGGCCAGT
                                                                       99.6%; Score 708; DB 22; I larity 100.0%; Pred. No. 2.1e-205; Conservative 0; Mismatches 0;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                            Db 128353 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGGGCGCTGGATCAACGTCGTGTC 128294
                                128474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                               009
                                                                                                                                                                                                                                                GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yokoi H;
541 ATTITCGCCGCTGGCGCTTCGCGGCAAGCCTGATCTGGTTCCCCGCTGGTGGGTTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                           Db 128293 GTGGCAGTTGTGATGACGCATTGGCCATCAAACTGATGTTGATGGCTTAG 128243
                                                                                                                                                                                                                                                                                                                                      GIGGCAGTIGIGATGACCGCATIGGCCATCAAACTGATGTTGATGGTTAG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO: 3455; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C glutamicum coding sequence fragment SEQ ID NO: 3455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH68420 standard; DNA; 708 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organic acid synthesis; ds
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P-PSDB; AAG93201.
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Tateishi D
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301 CCACAGATCATTGAAGAAACAGAACCGAACGTGCCCGATGACACGCCTTTGGGCGGGTTCG
                                                                                                            481 TTGGACGCGTTTGTGTTTTATCGGCGCGCGCGCGCAATACGGCGACACCGGACGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 GCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTC
                                                                      GCGGTGGCCACTGACACGCGCAACCGGGTGCGGGGGGTGAGCGTCGAGCGGTCGATAAGCAGCGG
                                                                                                                                                                                                                           421 GTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTTGACCTTGAACCCCGAATGCGTAT
                                                                                                                                                                                                                                                                                                                                  481 Tricaccirrirgretrirarcescescescescescescaracescescescescesces
                                                                                                                                                                             GTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCCGAATGCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat-resistant; lysin biosynthesis; enzyme; coryneform;
aspartate-semialdehyde dehydrogenase; lysE; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. thermoaminogenes lysin biosynthetic enzyme lysE DNA
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AAA52691;
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             1423
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                                                                                                                                                                                                                                                                                                                                                                         61 ATCGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                      GTTCTTCTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACAGATCATTGAAGAAACAAACCAACCGTGCCCGATGACACGCCTTTGGGCGGTTCG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                            898 drcarcarcirricrerereretedacidedecricirreacerecededecredadere 957
                                                                                                                                                                                   The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present sequence encodes an enzyme of the invention.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTTGGGGGCCAGTCTTTTACTGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCTTTTGTCCAATGCCGCCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 TACCTGCTGTGGTTCGCGGTGATGGCGGCGCGCGCGCCCTGCGCGCCCCGCACCGAGGTA
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                                                                                                                            of a high
                                                                                                                                                                                                                                                                               22; Length 1568;
                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                              Score 317.6; DB 22; Length
Pred. No. 2.8e-86;
0; Mismatches 214; Indels
                                                                                                                                gene
                                                                                                                                                                                                                                                        Sequence 1568 BP; 258 A; 525 C; 490 G; 295 T; 0 other;
                                                                                                                           heat-resistant lysin biosynthetic system enzyme
                                                                                                                                         temperature-resistant coryneform microbe
                                                                                                                                                             Example 5; Page 22-24; 27pp; Japanese.
                                                                                                                                                                                                                                                                               44.78;
                       99JP-0311148
                                              99JP-0311148
                                                                                                                                                                                                                                                                                                      Matches 481; Conservative
                                                                     (AJIN ) AJINOMOTO KK
                                                                                            WPI; 2001-364760/38.
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                        P-PSDB; AAG64047
                       01-NOV-1999;
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08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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The present sequence is the yggA gene (an excretion protein gene) of secherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion profein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 CTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTTTA 138
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                                                                                                                                                                                                                                                                                                                                                                                  production; excretion protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 TACTITICAAGGICTITGCACTITGGGGCGCTATGAICCTACCGCTCGGTCCACAAAIGCT
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11.1%; Pred. No. 4.3e-08;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakanishi K, Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 636 BP; 120 A; 143 C; 180 G; 193 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                B. coli; yggA gene; amino ació
amino acid excretion protein;
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                                                                                                                                                                                                                                                                                                                           Escherichia coli yggA gene
                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                      DNA;
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P-PSDB; AAB01789.
                                                                                                                                                                      AAA52691 standard;
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Tokhmakova IL;
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4792 AGGTCCTGGTGACCTGTGCGGCATTCACGTTCCTCAACCCACACGTCTACCTCGACACGC 4733

491 TIGIGITTATCGGCGCGTCGGCGCCCAATACGGCGACCGGACGGTGGATTTTCGCCG

4732 TCGTGTTGCTAGGCGCCTGGCCAACGAGCACAGCGA---CCAGCGCTGGCTGTTCGGCC 551 CTGCCGCGTTCGCGCCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCAT 4616

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4615 rececesererrerenceaececererereseaenen 4515 rececesereareseaenea 4556

4555 rahracracacradanterecerane 4523 TGATGACCGCATTGGCCATCAAACTGATGTTGA 703

AA199683 standard; DNA; 4403765 BP.

TGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG 670

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region results in an aviralence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33537) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an virulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletions are detected either by detecting the consense of deletion junctions (see AAT3538-46), or by detecting the presence or absence or absence or absence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
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199 GCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGTTTGCC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCG delta 2; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "BCG delta 1 deletion region"
                                                                                          259 GTCATGGCAGCGAAAGACGCCATGACAAACAAGGTGGA 296
                                                                                                                                       253 rrrggcgcrtrrraaaacagcaargagcagraararrga 290
                                                                                                                                                                                                                                                                                                                                                                                                        BCG deletion region 2 and flanking sequences.
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                                                                                                                                                                                                                                                                AAT33536 standard; DNA; 15239 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis strain BCG.
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Best Local Similarity 53.19
Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPI; 1996-393419/39.
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Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.

Mycobacterium tuberculosis.

US6294328-B1.

98US-0103840. 98US-0103840.

24-JUN-1998; 24-JUN-1998;

25-SEP-2001

(GENO-) INST GENOMIC RES

Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.

(first entry)

15-JAN-2002

AA199683;

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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium theorem. Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                              Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
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          Fraser CM, Venter JC;
Fleischmann RD, White OR,
                                                                                                    WPI; 2001-647261/74.
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8.0%; Score 57; DB 22; Length 4403765; 53.1%; Pred. No. 2.9e-05;

Query Match Best Local Similarity

1;

Gaps

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431 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 490

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Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

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Length 4411529;

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                                                                    2227633 AGGICCIGGIGACCIGIGGGGCATICACGIICCICAACCCACACGICIACCICGACACC 2227692
                                                                                                                                 2227693 TCGTGTTAGCGCGCGCTGGCCAACGAGCACAGCGA---CCAGCGCTGGCTGTTCGGCC 2227749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium thuserculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the uncleotide sequences of M. tuberculosis strains CDC 1551 (Ax199683) and H37Rv (Ax199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                            610
                                  431 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 490
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                                                                                                      491 TTGTGTTTTATCGGCGCGTCGCGCGCGCAATACGGCGACACCGGACGGTGGATTTTCGCCG
                                                                                                                                                                        551 CTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCCAGCAT
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 Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis;
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Conservative
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequata.uspto.gov/sequence.html?DocID=6294328B1.

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                                                                                                                                                                               Db 2230394 TCGTGTTGCTAGGCGCGCTGGCCAACGAGCACACGAA---CCAGCGCTGGCTGGTTCGGCC 2230450
                                                                                                         Db 2230334 AGGTCCTGGTGACCTGTGCGGCATTCACGTTCCTCAACCCACACGTCTACCTCGACACCG 2230393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                    610
                                                                       431 AGCCCATGTTGATGGCAATCGTGCTGACCTGAACCCGAATGCGTATTTGGACGCGT 490
                                                                                                                                             491 TTGTGTTTTAFCGGCGGCGTCGGCGCATACGGCGACACACGGACGGTGGATTTTCGCCG 550
                                                                                                                                                                                                                                                                                        611 TGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG 670
                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                     3;
Score 57; DB 22; Length 44
Pred. No. 2.9e-05;
0; Mismatches 125; Indels
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 8.0%;
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23-AUG-2000; 2000US-0649167.
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                                   Matches 145; Conservative
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                  Similarity
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

invention relates to isolated polynucleotide (I) and

Claim 1; SEQ ID No 30055; 103pp; English.

biodiversity

polypeptide (II) sequences. (I) be useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and administration acid sequences. AASS4197-AASS4564 represent novel human

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diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO

ftp.wipo.int/pub/published_pct_sequences.

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a food supplement. [1] and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of deta and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human when the product coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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   quantitating a polypeptide in tissue, as molecular weight markers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 AACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTTTAATTTCTGACG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Local Similarity 48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                   89 AACAAGGAATTAAGCGCGAAGGACTCATTGCGGTTCTTCTCGTGTTTAATTTCTGACG 148
                                                                                                                                                                                                                                                                                                                                                                                           209 IGCTCGATATTATGCGCTGGGTGGCATCGCTTACCTGTTATGGTTTGCCGTCATGGCAG
                                                                                                                               29 GICTGCTTTTGGGGGCCAGTCTTTTACTGTCCATCGGACCGCAGAATGTACTGGTGATTA
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                                                                                                                                                                                                                                                                                                      149 TCTTTTTGTTCATCGCGGCACCTTGGGCGTTGATCTTTTGTCCAATGCCGCGCGCATCG
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                                          6.7%; Score 47.4; DB 23; Length 7521; 48.4%; Pred. No. 0.0012;
Sequence 7521 BP; 1896 A; 1856 C; 2100 G; 1669 T; 0 other;
                                                                                      0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4734 GGAAGAAGAGACGGAAGAAGGAGGAGAGAAGC 4766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 CGAAAGACGCCATGACAAACAAGGTGGAAGCGC 301
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AAF71777 standard; DNA; 993
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                                                                                    Matches 132; Conservative
                                                              Local Similarity
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New isolated polynucleotide and encoded polypeptides, useful in

Tang YT;

WPI; 2001-639362/73. P-PSDB; ABG30064. Drmanac RT, Liu C, (HYSE-) HYSEQ INC

Gaps

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Indels

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Metabolic pathway protein; MP; lysine biosynthesis pathway;
methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins of the invention fantly about 22). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polynucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
                                                                        AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
                                                                                                                                                                                                Score 39; DB 22; Length 993;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                           C. glutamicum gene #21 encoding metabolic pathway protein.
                                                                                                                                                                         Sequence 993 BP; 233 A; 256 C; 268 G; 236 T; 0 other;
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100.0%; Pred. No. v..
'.. 0; Mismatches
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                                                   Claim 3; Page 226-228; 1737pp; English.
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                                                                                                                                                                                                                                                                                                              RESULT 14
AAS96096/c
ID AAS96096 Btandard; DNA; 993
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23-JUN-2000; 2000US-0606740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum.
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Matches 39; Conservative
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Lee H, Hwang B;
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99DE-1031428.
99DE-1031434.
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99DE-1031420
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   WO200100843-A2.
                                                   23-JUN-2000;
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                            04-JAN-2001
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Kim J;

Haberhauer G,

Nucleic acids from Corynebacterium glutamicum encoding metabolic

WPI; 2001-137957/14. P-PSDB; AAB79658.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of the tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequata uspto.gov/sequence.html?DocID=6294328B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                                                                      Gaps
AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis, strain H37Rv, strain CDC 1551, genome, variation, epidemiology, patient treatment, epidemio monitoring, d
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                                                                                             DB 23; Length 993; 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
                                                                                                                                    Indels
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                                                      Sequence 993 BP; 233 A; 256 C; 268 G; 236 T; 0 other;
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                                                                                                                                                                      1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTG 39
                                                                                                                                                                                           39 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTG 1
                                                                                           Query Match 5.5%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 39; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                   AAI99683 Btandard; DNA; 4403765 BP
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AAI99683/c
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Gaps

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0; Mismatches 124; Indels

Length 4403765;

DB 22;

Score 37.6; 1 Pred. No. 23;

Query Match 5.3%; Best Local Similarity 47.5%; Matches 112; Conservative 430 AAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCG 489

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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
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'ptodata/2/pubpna/USOG_NEW_PUB.seq:*
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

APPLICANT: Hwang, Byung-Joon TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

FILE REFERENCE: BGI-121CP2

Schroder, Hartwig Zelder, Oskar Haberhauer, Gregor Kim, Jun-Won Lee, Heung-Schick

> APPLICANT: APPLICANT: APPLICANT:

Kroger, Burkhard

ompejus, Markus

CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR PILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-12
PRIOR PILING DATE: 1999-06-12
PRIOR PILING DATE: 1999-09-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 1999-09-12
PRIOR PILING DATE: 1999-09-12
PRIOR PILING DATE: 1999-09-12
PRIOR PILING DATE: 1999-07-08

TYPE: DNA ORGANISM: Corynebacterium glutamicum

SEQ ID NO 51 LENGTH: 822 NAME/KEY: CDS LOCATION: (101)..(799) OTHER INFORMATION: RXA01394

Sequence 1, Appli Sequence 19241, A Sequence 2513, Ap Sequence 20241, A Sequence 2171, Ap Sequence 4, Appli Sequence 760, App Sequence 198, App Sequence 1, Appli Sequence 3455, Ap Sequence 11, Appl Appli Sequence 51, Appl Sequence 12392, Sequence 439, A Sequence 346, Sequence 346, Sequence 47 Sequence 1 Description Sequence 1 US-09-738-626-1 US-10-184-634-346 US-10-184-634-346 US-09-430-029-1 US-09-974-300-2171 US-09-796-679-4 US-09-926-300-760 US-09-976-059-1 US-09-976-059-1 US-09-738-626-439 US-09-864-761-19241 US-09-864-761-2513 US-09-864-761-20241 US-09-738-626-1 US-09-738-626-3455 US-09-894-844-11 US-09-746-660A-47 US-09-746-660A-51 Query Match Length DB 100.0 100.0 99.6 Score 37.2 Result No.

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	77	33.4	4.7	412	σ	US-09-918-995-36145	
U	55	33.2	4.7	160	10	US-09-923-876-582	e 582,
	23	33		446	10	US-09-864-761-20699	Sequence 20699, A
	24	32.8	4.6	443	6	US-09-918-995-13829	Sequence 13829, A
υ	25	32.8	4.6	443	σ	US-09-918-995-20282	Sequence 20282, A
	56	32.8	4.6	479	6	US-09-918-995-31047	Sequence 31047, A
	27	32.8	4.6	562	6	US-09-918-995-37138	Sequence 37138, A
	28	32.8	4.6	2209	10	US-09-726-397A-2	Sequence 2, Appli
Ö	53	32.8	•	2366	2	US-09-726-397A-3	Sequence 3, Appli
	30	32.8	4.6	2568	6	US-09-738-626-15	Sequence 15, Appl
	31	32.8	•	3955	٥	US-10-219-248-4	Sequence 4, Appli
	32	32.8	•	3955	σ	US-10-219-247-4	Sequence 4, Appli
	33	32.8	•	3955	2	US-09-855-722-4	Sequence 4, Appli
	34	32.8	•	4702	10	US-09-880-107-1545	Sequence 1545. Ap
	35	32.8	•	62944	10	US-09-954-456-2257	Sequence 2257, Ap
	36	32.6	•	520	δ	US-10-184-644-332	Seguence 332, App
	37	32.6	4.6	520	σ	US-10-184-634-332	Sequence 332, App
υ	38	32.6		1164	0	US-09-712-363-110	Sequence 110, App
	39	32.6	4.6	3627	σ	US-09-927-827-4	Sequence 4, Appli
	40	32.6		7356	σ	US-09-927-827-1	Sequence 1. Appli
ט	41	32.4		497	თ	US-09-918-995-27219	
	42	32.4	4.6	591	10	US-09-833-381-112	a
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	40	32.4	4.0	3478	ת	US-09-991-053-3	Sequence 3, Appl1
						ALIGNMENTS	
RES	RESULT 1						
us.	-09-74	US-09-746-660A-51	ed.				
	Sequen	Sequence 51, Application US/09746660A	pplica	tion US	/097	46660A	
	Public RENERA	Publication No. US20030049804A1 GENERAL INFORMATION:	US20	0300498	04A1		

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                                                                                                                                                                                           ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG 211
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                                                                                              ATGGTGATCATGGAAATCTTCATTACAGGTCT@CTTTTGGGGGCCAGTCTTTTACTGTCC
                                                                                                                                                                                                                                                                                          GATCTTTTGTCCAATGCCGCCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
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                                                              Indels
                            ; Score 711; DB 9;
; Pred. No. 7.9e-232;
0; Mismatches 0;
                                100.0%;
                            Query Match
Best Local Similarity 100.
Matches 711; Conservative
US-09-746-660A-51
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Db 1328773 GATCTTTTGTCCCAATGCCGCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT 1328714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 1328473 TTGGACGCGTTTGTTGTTTATCGGCGCGTCGGCGCGAAAACGGCGACACCGGACGGTGG 1328414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1328413 ATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGC 1328354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 1328953 ArGGrGArCArGGAAArCTrCATrACAGGrCrGCTrTrGGGGGCCAGrCTrTrACTGTCC 1328894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1328893 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCCGCGAAGGACTCATTGCG 1328834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 1328833 GTTCTTCGTGTGTTTAATTTCTGACGTCTTTTTGTTCATCGCCGGCACCTTGGGCGTT 1328774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1328653 CCACAGATCATTGAAGAAACAAAACCAACCGTGCCCGATGACACGCCTTTGGGGCGGTTCG 1328594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1328533 GTTTGGGTAAAGCCCATGTTGATGGCAATGGTGACCTGACTTGAACCCGAATGCGTAT 1328474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1328353 GCAGCAGCATTGTCACGCCCGCTGTCCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTC 1328294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CCACAGATCATTGAAGAAACAGAACCAACGTGCCCGATGACACGCCTTTGGGGCGGTTCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAGGACTCATTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GATCTTTTGTCCAATGCCGCCGATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 711; DB 9; Length 3. Best Local Similarity 100.0%; Pred. No. 6.4e-230; Matches 711; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGTGATCATGGAAATCTTCATTACAGGTCTGCTTTTTGGGGGCCAGTCT
CURRENT FILING DATE: 2000-12-18
PRICR APPLICATION NUMBER: JP 99/377484
PRICR FILING DATE: 1999-12-16
PRICR FILING DATE: 1999-12-16
PRICR FILING DATE: 2000-04-07
PRICR FILING DATE: 2000-08-03
PRICR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NOS: 7059
SEQ ID NO 1
LENGTH: 3309400
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; ORGANISM: Corynebacterium glutamicum US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-738-626-3455
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Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKGARA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: TATEISHI, NAKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
US-09-738-626-1/c
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   491 TTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGCGACACCGGACGGTGGATTTTCGCCG
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differences Between Species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.0%; Score 57; DB 9; Length 597; Best Local Similarity 53.1%; Pred. No. 4.9e-09; Matches 145; Conservative 0; Mismatches 125; Indels
                                                                                                                                            661 GTGGCAGTTGTGTGACCGCATTGGCCATCAAACTGATGTTGATGGGT 708
                                                                                                       661 GTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Behr, Marcel
APPLICANT: Behr, Marcel
APPLICANT: Small, Peter
APPLICANT: Schoolink, Gary
APPLICANT: Schoolink, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between S;
TITLE OF INVENTION: the M. Tuberculosis Complex
FILE REPERENCE: STANIO2CON
CURRENT APPLICATION NUMBER: US/09/894,844
CURRENT FILING DATE: 1999-05-27
PRIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-08-25
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SCBTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 597
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Publication No. US20030049804A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Kim, Unn-Won
APPLICANT: Kim, Unn-Won
APPLICANT: Lee, Heung-Schick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Mycobacteria tuberculogis
US-09-894-844-11
                                                                                                                                                                                                                                                                                                                            ; Sequence 11, Application US/09894844; Patent No. US20020176873A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-746-660A-47/c
                                                                                                                                                                                                                                                                                                  JS-09-894-844-11
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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US-09-738-626-3455
                                 MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                   HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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SEQ ID NO 3455
LENGTH: 708
NAKAGAWA, SATOSH
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Best Local Similarity 100.
Matches 708; Conservative
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469 CCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGCGTCGGCGCGCAATACGGCGAC 528
                                                                         181 TCGAAGGCGCCGGTGGCCTCGTCGAAGCTGTAGGAGGTGACGAGTCCGGGATGAGCCCC 122
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Pred. No. 0.095;
0; Mismatches 65; Indels
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/28098
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                       529 ACCGGACGGTGGATTTTCGCCGCTGGCGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09738626
5. US20020197605A1
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Publication No. US20020197605A1
GENERAL INFORMATION:
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Best Local Similarity 53.6%;
Matches 75; Conservative
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MIZOGUCHI, HIROSHI
ANDO, SEIKO
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ANDO, SEIKO
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 439
LENGTH: 1068
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TATEISHI, NAOKO
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SENOH, AKIHIRO
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Pred. No. 0.023;
0; Mismatches 118; Indels
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OTHER INFORMATION: Clone ID: 53-LIB3058-002-Q1-K1-F2
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Fatent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wealey C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WUCKEIC ACID AND OTHER MOLECUI
TITLE OF INVENTION: WUCKEIC ACID AND OTHER MOLECUI
TITLE OF INVENTION: WUCKEIC AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NO 12392
LENGTH: 424
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100.0%; Pred. No. 0.0087;
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METABOLIC PATHWAY PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                             CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR PILING DATE: 2000-6-23
PRIOR PILING DATE: 2000-66-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR APPLICATION NUMBER: 09/603124
PRIOR PILING DATE: 1999-60-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/18790
PRIOR APPLICATION NUMBER: 01999-08-12
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATENTIN VOTES: 2.0
                                        FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
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Best Local Similarity 47.8%;
Matches 108; Conservative
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; OTHER INFORMATION: RXA01393
US-09-746-660A-47
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Matches 39; Conserva
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LENGTH: 993
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92 YSAPPPVSSDSEAPEANPADGSDADEDDEDKGVMAVTATAASDRMESDSDSDKSSD 151
                                                                                                               112 VRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMARSASSSSSSSSSSSDSDVSVK 271
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
    168 CACCTIGGGCGTIGAICTTTTGTCCAATGCCGCCGATCGTGCTCGATATTATGCGCTG 227
                                                                                                                                                                                                                                                                                        408 CGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAA 467
                                                                                                                                                                                                                                                                                                                                                                         348 TTTGGCCGCTCCGCCGCCACTGACACGCGCAACCGGGTGCCGGTGGAGGTGAGCGT 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 CACCTTGGGCGTTGATCTTTTGTCCAATGCCGCCCGATCGTGCTCGATATTATGCGCTG 227
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 346, Application US/10184634; Publication No. US20030068684A1; GENERAL INFORMATION:
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Wood, William I.
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Best Local S:
Matches 29,
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APPLICANT:
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CURRENT APPLICATION NUMBER: 105/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 9
Pred. No. 6.6;
0; Mismatches
                                                        CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PLILING DATE: 1999-12-16
PRIOR PLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PLICATION NUMBER: UP 00/28098
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
OZAKI, AKIO
ENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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Wood, William I.
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Best Local Similarity 53.64
Matches 75; Conservative
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Godowski, Paul J
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Smith, Victoria
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                   TITLE OF INVENTION: NOV FILE REFERENCE: 249-125
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LENGTH: 671
                                                                                                                                                                                                                                                                          SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Length 671; Indels

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5710 CCGCCGGGAACCCGGATGTACCGCACCGGCGATCTTGCCCGCAGGCGCCCAGGACGGTCT 5769
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                                                                                                                                                                                                                                                                                     441
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                                                                                                                                            322 GAACCAACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGGCCACTGACACGCGC 381
                                                                        Gaps
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; Sequence 2171, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REPERENCE: 10085.500.US
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-3-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: PEAUSEC for Windows Version 4.0
Length 5828
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; Score 35; DB 9; Pred. No. 0.51; 0; Mismatches
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Pred. No. 0.
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FILE REFERENCE: 23607 MRB
FURENT APPLICATION NUMBER: US/09/796,679
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09796679
Publication No. US20030013076A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Bacillus licheniformis
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APPLICANT: Lyttle, David J
APPLICANT: University of Otago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.9%;
Query Match
Best Local Similarity 50.3%;
Matches 86; Conservative
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Matches 69; Conserva
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LENGTH: 7158
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Sequence 1, Application US/09430029;
Fatent No. US20020168738A1
SEQUENCEL INFORMATION:
APPLICANT: Vano, Tetauya; No. US20020168738A10to, tauyoshi; Imamura, Takeshi; C
TITLE OF INVENTION: Becombinant Plasmid, Transformed Microorganism,
TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Method for Environmental Remediation
FILE REPERENCE: CF013982US
CURRENT APPLICATION NUMBER: US/09/430,029
CURRENT FILING DATE: 1999-10-29
EARLIER RPLING DATE: 1999-10-30
NUMBER OF ECO ID NOS: 13
                                                                                                                                                                                                                                                                                  CGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAA 467
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                                           TTTGGGCGGTTCGGCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGT 407
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   272 KPPRGRKPAEKPLPKPRGRKPKPERPPSSSSDSDSDEVDRISEWKRRDEARRELEARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 CACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAG 569
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INFORMATION: tomM
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INFORMATION: tomN
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INFORMATION: tomO
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; OTHER INFORMATION: tomQ
US-09-430-029-1
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THER INFORMATION: tomK
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OTHER INFORMATION: tomL
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LENGTH: 5828
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Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                   DB 10; Length 2048;
                                                                                                                      50; Indels
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APPLICATION NUMBER: US/09/745,763
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Pred. No. 0.91;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                         0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 198:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               Score 34;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 198, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 41,33
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LENGTH: 2930 base pairs
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STRANDEDNESS: double
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                                                                                                                      64; Conservative
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Best Local Similarity 49.7
Matches 86; Conservative
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                                                                             Best Local Similarity
Matches 64; Conserv
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APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.4; DB 9; Length 4 Pred. No. 0.7; 0; Mismatches 191; Indels
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PRIOR APPLICATION NUMBER: PCT/NZ97/00040 BRIOR FILING DATE: 1997-03-27 PRIOR APPLICATION NUMBER: NZ 286284 PRIOR FILING DATE: 1996-03-29
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Patent No. US20020151681A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc feature
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                                                                                                                                    NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2
SEQ ID NO 4
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LENGTH: 2048
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Search completed: April 27, 2003, 04:41:53 Job time : 2873.3 secs

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Sequence 34, Ap
Sequence 5, App
Sequence 19, Ap
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-103-840A-2

US-09-103-840A-1

US-08-38-08-28-2

US-08-58-004-2

US-08-402-066-2

US-08-402-066-2

US-09-44-288-7

US-09-13-288-7

US-09-14-278-4
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US-08-804-227C-1
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US-08-078-271B-9
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US-08-611-729A-7
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                                                                OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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APPLICANT: Stover, Charles K.
APPLICANT: Stover, Gregory G.
APPLICANT: VINUENCE-ATTENUATING GENETIC DELETIONS
TITLE OF INVENTION: URULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Ploor
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,878

FILING DATE: 17-FEB-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION UNMBER: 38,498

REGISTRATION NUMBER: 38,498
US-08-997-080-153

US-08-997-362-153

US-09-095-855-153

US-09-324-542-153

US-09-204-796-17

US-09-119-892-1

US-09-119-892-1

US-09-119-892-1

US-09-118-817-9

US-09-118-817-1

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US-09-018-817-1

US-09-018-817-1

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Patent No. 5700683
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/5600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Best Local Similarity 53.1
Matches 145; Conservative
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STATE: California
COUNTRY: USA
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OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

CS-09-103-840A-2
                                                                                             4732 TCGTGTTGCTAGGCGCGCTGGCCAACGAGCACAGCGA---CCAGCGCTGGCTGTTCGGCC 4676
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APPLICANT: FRASER, Claire M.
APPLICANT: VERSER, Claire M.
APPLICANT: VENTER, Cohn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
TGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG
                                                                                                                                                                                                     TCCCGCTGGTGGGTTTCGGCGCAGCAGCAT
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Pred. No. 6.9e-06;
0; Mismatches 125; Indels
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity 53.1%;
Matches 145; Conservative (
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US-09-103-840A-2
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Sequence 1, Application US/09103840A Patent Nd. 6294328 GENERAL INFORMATION:

RESULT 3 US-09-103-840A-1

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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 490
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APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: HITE, Owen R.
APPLICANT: HITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UNBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                               FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       611 TGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 4; Le
Pred. No. 6.9e-06;
0; Mismatches 125;
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APPLICANT: FRASER, Claire M.
TTILE OF INVENTION: DOIN C.
TILLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNDBER: US/09/103,840A; CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 TGATGACCGCATTGGCCATCAAACTGATGTTGA
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%;
53.1%;
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Best Local Similarity 53.1
Matches 145; Conservative
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4.9%; Score 34.6; DB 1; Length 6611; 50.3%; Pred. No. 1.7;
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OTHER INFORMATION: /function= "coding sequence"
OTHER INFORMATION: /function= "coding sequence"
OTHER INFORMATION: /froduct= "DNA polymerase"
NAME/KEY: misc_feature
LOCATION: 2107..3132
OTHER INFORMATION: /function= "potential open reading oTHER INFORMATION: frame"
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LOCATION: 3138..3359
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5028..5375
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5375.5653
CTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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GTHER INFORMATION: /function= "potential open reading of the control of th
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
STREST: 1 Becton Drive
CITY: Pranklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-326
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6611 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 4690..5028
OTHER INFORMATION: /function=
OTHER INFORMATION: frame"
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MOLECULE TYPE: DNA (genomic)
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NAME/KEY: misc feature
LOCATION: 5653.5910
OTHER INFORMATION: funct
OTHER INFORMATION: frame"
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TYPE: nucleic acid
STRANDEDNESS: double
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Franklin Lakes
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                 Db 720383 GGGCTGCTGCTCCTGCAACGGGGGGGGACGACGAATGTTCGGGGGTCACCGACCACGAC 720324
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430 AAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCCGAATGCGTATTTGGACGCG 489
                                                                                                                                                                                                                                                                                                   GCTGGCGCTTCGCGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 AAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGGAATGCGTATTTGGACGCG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 TTTGTGTTTATCGGCGGCGTCGGCGCCAATACGGCGACACCCGGACGGTGGATTTTCGCC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 720263 GAGATCGGCCCGGTCGCGGCCACACGCGTTGCACGGGTTTACCGCGTCGATGGC 720208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                 610 TIGICACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGC 665
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Pred. No. 4.7;
0; Mismatches 124; Indels 0;
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Hamilton, Paul T.
Little, Michael C.
Beyer Jr., Warpe F.
VENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
VENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09103840A Patent No. 6294328
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Patent No. 5476768
GENERAL INFORMATION:
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Best Local Similarity 47.5%;
Matches 112; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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Best Local Similarity 50.3%; Pred. No. 1.7;
Matches 85; Conservative 0; Mismatches 84; Indels 0
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Patent No. 5612182
GENERAL INFORMATION:
APPLICANT: Peatenn, Robert B.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             739 recedenaeracecedeceracecenedades
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 5028..5375
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY:
NEORWATION: frame"
                              FEATURE:
NAME/KEY: misc_feature
LOCATION: 4690..5028
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 5653..5910
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature;
| IOCATION: 6078..6491
| OTHER INFORMATION: /function= "potential open reading | OTHER INFORMATION: frame"
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402.066
       OTHER INFORMATION: frame'
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CITY: Franklin Lakes
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COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
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ADDRESSEE:
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                                                                                                                                                                                                                          GGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCCGAATGCGT 478
       0; Gaps
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LOCATION: 2107..3135
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3138..3359
OTHER_INFORMATION: /function= "potential open reading
84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE:
NAME/KEY: misc_feature
LOCATION: 390.1538
OTHER INFORMATION: /function= "coding sequence"
OTHER INFORMATION: /product= "DNA polymerase"
FEATURE:
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APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: FCBLELLIAN ACCOUNTERNT APPLICATION NUMBER: US/08/508,004
PILING DATE: 27-UL-1995
CLASSIFICATION NUMBER: US/08/508,004
PILING DATE: 27-UL-1995
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: FUGIT NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 2,135
REFERENCE/DOCKET NUMBER: 19-3283
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08508004
Patent No. 5582969
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
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MOLECULE TYPE: DNA (genomic)
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CITY: Franklin Lakes
Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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Matches
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COUNTRY:
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4.9%; Score 34.6; DB 1; Length 6611;
Best Local Similarity 50.3%; Pred. No. 1.7;
Matches 85; Conservative 0; Mismatches 84; Indels 0
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NAME/KEY: misc feature
LOCATION: 5175..5653
OTHER INFORMATION: /function= "potential open reading
FRATURE:
NAME/KEY: misc feature
LOCATION: 5553..5910
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAMEKKEY: misc_feature
LOCATION: 4690.:5028
OTHER INFORMATION: frame" "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 2107..3132
OTHER INFORMATION: /function= "potential open reading OTHER:
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LOCATION: 3138..3359
OTHER INPORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5028..5375
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 390.1538
OTHER INFORMATION: /function= "coding sequence"
OTHER INFORMATION: /product= "DNA polymerase"
FILING DATE:
CLASSIFICATION: 436
ATTORNEY, PAGENT INPORMATION:
NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 32,135
REGISTRATION NUMBER: 32,135
REGISTRATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6611 base pairs
TYPE: nucleic acid
STRANDENRES: double
TYPE: nucleic acid
STRANDENRES: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
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RESULT 9

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SEGUENCE 2. APPLICATION US/08402068
PARTICUM: PRATEON Robert E. APPLICANT: PRATEON ROBERT C. MANUE P. STAILS OF COURSESIES.

MAPPLICANT: BARGEN ROBERS S. TITLE OF INTENTION WYCOBACTERIUM TUBERCULOSIS COMPLEX COURSESSURES. Company WYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEGUENCES. G. COMPANY S. SEGUENCES. G. SEGUENCES. G. COMPANY S. SEGUENCES. G. SEGUENCES. SEGUENCES. G. SEGUENCES. SEGUENCES.
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US-09-214-278-4
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SEQ ID NO 4
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APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
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4.9%; Score 34.6; DB 1; Length 6611;
Best Local Similarity 50.3%; Pred. No. 1.7;
Matches 85; Conservative 0; Mismatches 84; Indels 0
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LOCATION: 6078..6491
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
    /function= "potential open reading
frame"
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4.7%; Score 33.6; DB 4;
Best Local Similarity 49.4%; Pred. No. 1.8;
Matches 87; Conservative 0; Mismatches 89;
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; ORGANISM: Streptomyces narbonensis
US-09-434-288-7
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Patent No. 6303767
GENERAL INFORMATION:
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APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
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SOFTWARE: PatentIn Ve
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Microbial System for Formaldehyde Sensing and
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Patent No. 6291210
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Itch, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
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0; Mismatches 120;
                                                                                                  TILE REFERENCE: 96026.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/608,241
EARLIER PILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 4826
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; LOCATION: (2236)..(4437)
US-09-192-983-3
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LOCATION: (993)..(2165)
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: (12) .. (89)
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ORGANISM: Homo sapiens
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LOCATION: (215)..(895)
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Best Local Similarity
Matches 105; Conserv
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Sequence 7, Application US/08611729A
Patent No. 6004924
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STREET: 11
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; LOCATION:
US-08-611-729A-7
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                                                                    378 GCGCAACCGGGTGCGGTGGAGGTGAGCGTCGATAAGCAGCGGGTTTTGGGTAAAGCCCCAT 437
                                        Gaps
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       DB 4; Length 3955;
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Nucleic Acids and Methods of Use
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Proceeding 1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
***RILING DATE: 25-JUN-1997
                                                                                                                                                                    3413 ccGcaaccccarcaaccccacacacacacacara 3452
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                                      42;
                                                                                                                                         GCTGACCTGGTTGAACCCGAATGCG 477
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     Score 32.8; Di
Pred. No. 4.6;
O; Mismatches
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Pred. No. 4.8;
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Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged P
TITLE OF INVENTION: Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-UTN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPRENCE/DOCKET NUMBER: P-UW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEG ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 4315 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
     4.6%;
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Best Local Similarity
Matches 58; Conserv
                   Similarity
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Query Match
Best Local
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RESULT 14

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Sequence 34, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3163 GAGGAGCCGGCTGCCGCGGGAGGAGCGCCAACAACCAGTGGGCCCCGCTCAACCCCAT 3222
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                                                                                                                 APPLICANT: Fleming, Robert J.
APPLICANT: Artavanie-Tsakonas, Spyridon
APPLICANT: Artavanie-Tsakonas, Spyridon
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3223 CCGCAACCCCATTGAGCGGCCGGGGGGCCACAAGGACGTG 3262
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58.0%; Pred. No. 4.9;
tive 0; Mismatches
                                                                                          Myat, Anna M.
Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
Mann, Robert S.
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                      Ish-Horowicz, David
Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 73
IELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pair
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EDNESS: single
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Matches 58; Conserv
GENERAL INFORMATION:
APPLICANT: ISh-Ho
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                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                             New York
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ADDRESSER SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza
CITY: Garden City
COUNTR: WAS
COUNTR: WAS
COUNTRE. WY
COUNTR: WAS
COUNTRE. WAS
SOFTWARE: PACENT NECESSER #1.0, Version #1.25
CUARRY APPLICATION NUMBER:
APPLICATION NUMBER: 1,346
REGISTRATION FOR WAS
TELEBRAM: 216-742-436
TELECOMMUNICATION NUMBER: 31,346
REGISTRATION NUMBER: 1,346
REGISTRATION NUMBER: 1,346
REGISTRATION NUMBER: 1,346
TELEBRAM: 516-742-436
TELEBRAM: 110-14-14-14
TELEBRAM: 110-14-14
TELEBRAM: 110-14-14-14
TELEBRAM: 110-14-14
TELEBRAM
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Search completed: April 27, 2003, 03:47:50 Job time: 10403.1 secs

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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April 26, 2003, 18:49:18; Search time 2249.77 Seconds (without alignments) 11293.030 Million cell updates/sec
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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vrijic,m., sanm,H. and Eggeling,L. Pred. No. is the number of results predicted by chance to have a

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	ט ני		2,0	65.1	543980		AX1214/		AX12/14/ Sequence
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	7		326	37.3	822		AX063771		AX063771 Sequence
	200		976	37.3	822		AX244059		AX244059 Sequence
	101		9.0	22.2	1771		AB083133		AA123539 Sequence
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			9.6	15.6	13051		AE009111 SC7H9		AE009111 Agrobacte
_			115	13.2	306250		SME591788		ALS91788 Sinorhizo
			9.6	10.1	10871		965		AE011965 Xanthomon
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	7 8 0		٠. د د	α 4. υ	190050		AL646059		AL646059 Ralstonia
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	31,		9.1	8.5	5541		AR068500		AR068500 Sequence
	32		9.	800	5541		AX343066		AX343066 Sequence
	34		9.1	0 00	5541		AX347518 AX347541		AX34/518 Sequence
	35		1.6	8.5	5541		AX347564		AX347564 Sequence
			9.6	7.5	33285		SCSF8		AL357613 Streptomy
_	c 37		4.	7.5	988		AX431662		AX431662 Sequence
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	ACCESSION		X964	ucamic 71	um 1yBr	and a	l iyse genes.		
	VERSION		X964 1vsE	71.1 gene:	X96471.1 GI:17297	29753 gene:	. Lygine export	redulator	protein: Lysine
	SOURCE		exp Cory	exporter proteir Corynebacterium	rotein; erium o	t t	ine gove		
	ORGANISM	NISM	Cory	Corynebacterium	erium c	1) ut	glutamicum		
			Acti	nomyce	Actinomycetales; Cory	Sor	orynebacterineae;	įŪ	eriaceae;
_	REFEREN		701-	mebacte (bases 1	rium to	2374)			
_	AUTHORS		vrıj	Vrljic, M.,	Sahm	•	and Eggeling, L.		

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AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGGCGTCGGCGCGCAATACGGC 1540
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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PSYSIINRWYEEPGDGENILOSAANNGLGYTAFSPLAQGILTDKYLDGIPEGSRASO
PSYSIINRWYEEPGDGENILOSAANNGLGYTAFSPLAQGILTDKYLDGIPEGSRASO
SKSLSEGMINVNNIDMVRKINDIAQERGQSLAQMALAWYLREQGEYGADTVTSALIGA
SSYEQLONGLOSLNNILEFSDAELEAIDEISHDAGINIWAKATDSKTREN"
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640 g
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KVUVSRTQPRKATEAGEVUVQARKMVLLQAETKAQLSGRLAEIPLTTAINADSLSTW
RPPVFNEVASWAGGATUTLERLEDEAHTLISLLERGDVLGAVTREANPVAGCEVVELGTMR
HLALAFDSLRDAYMVDGKLDMAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPS
AEGFGEAIRRGLGWGLLPETQAAPMLKAGEVUILLDEIPDYPMYWQRWRLESRSLARL
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ETBPTVPDDPTPLGGSAVATDTRNRVRVEVSVDKQRVWYKPMLMAIVLTWINPNAYLDA
FVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSFKVWRWINVVV
AVVMTALAIKLMLMG"
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                                                                            2 (bases 1 to 2374)
Vrljic,M.M.
Direct Submission
Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
A new type of transporter with a new type of cellular function:
L-lyaine export from Corynebacterium glutamicum
Mol. Microbiol. 22 (5), 815-826 (1996)
97126810
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4.7e-185;
                                                                                                                                                                                                                                                                                                                                              /product="Lygine export regulator protein"
| Protein id="CaA65323.1"
| db_xref="G1:1729754"
| db_xref="SWISS-PROT:P94632"
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'db_xref="SWISS-PROT:P94633"
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; Pred. No. 4.7e
0; Mismatches
                                                                                                                                                                                       /organism="Corynebacterium
/strain="R127"
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/protein_id="CAA65325.1"
/db_xref="G1:1729756"
/db_xref="SPTREMBL:P94634"
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                                                                                                                                                                                                                                                                                  /gene="lysG"
/note="Lysine governor"
/codon start=1
/transl_table=11
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/gene="orf3"
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complement(82..954)
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|transl_table=11
|product="Lysine
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/gene="lysE"
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Matches 873, Conservative
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GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTCGCGGCAAGCCTGATCTGGTTCGCG
                                                                                               CTGGTGGGTTTCGGCGCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGC
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Corynebacterium glutamicum
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
Actinomycetales, Corynebacterineae, Corynebacteriacese;
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1 (bases 1 to 2374)
Velijc,M. and Eggeling,L.
PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS B
ACTIVITY OF EXPORT CARRIERS
PACENT: WO 9722597A 2 03-JUL-1997;
KERNFORSCHUNGSANLAGE JUELICH (DE); VRLIJC MARINA (DE)
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/organism="Corynebacterium glutamicum"
/db_xref="taxon:1718"
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iive 0; Mismatches 0;
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RESULT 3

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WALGITYTVILAALSI-FRSMCSIASKONYOKKYI YLSONYOK YSALOLOVAALFIKO
AIAIFIGSHSPTRVILAALVI-FRSMCSIASKONYOKKYI SKGKRGIAVTGRATYI GGVMGIVAGA
AIAICDKRAFREVILASMMLVTALSTRFIVALAAESGNSI IDSIGFFILASGIASMVGG
RISGINGSKAVRROGALFGSI VILILVVILSSAFAPAQINTLVFPILASGIASMVGG
IRVARKTYNMDMAEDORITRYVADANTLMGVVLLI VGALSGFFILI FGNEAALIFLAAI
AP005277 333150 bp DNA linear BCT 08-AUG-2002 Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section
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DVINNLDEMTTVHWHGMKLPAIADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHG
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EPQDRTTLALGPGERWEIVVELEPGEBVTLESVGFEDNYGYPDDEFVPDFGMSDSFQL
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AVEFGHYPDPQWPYMYHCHMLYHEDQGMMGQFVIVEPGBEPAAVLGSGTGSSIDSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLLALLVPIRBAGSMLPQAAITGWVLRQTSRSKVWVIGSNGQFVSALGIGVAALFLRG
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                                                                                                                                                                                                                                                                                                                                                       Nakagawa, S.
Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
Unpublished
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TIGR00960:3a0501s02: Type II (General) Secretory Pathway
(IISP) Family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co. Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 144-829-3031, Faril:snakagawa@xanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitagato University.
                                                                                                                                                                                            Corynebacterium glutamicum ATCC 13032 (strain:ATCC 13032) DNA. Corynebacterium glutamicum ATCC 13032) Bacteria; Actinobacteria; Actinobacteridae; Actinobacterides; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Corynebacterium glutamicum ATCC 13032"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="ATCC 13032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Gg10945"
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                                                                                          AP005277 BA000036
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/trānslation="MTAWLCSFPSGYQDEYDMANGVVQPQEHLDATLIAADFHGNPEN
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LASDSTEIIANLVRDEVNQYVPEDQSHVVNGVIDSIAGSAAAGQVGVAVGVITALWTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYVRAFSRCANAVYGRSEGRTLIKRWAMLLFLNLALLLGIIIILVSWVLNETLVWGIF
APIAEPLHLTNVLSFLTDRPMPIMIWVRFPVIVGVLIMFVATLYYWAPNARPWKFRWL
SLGSFLAIVGILLAGVGLNPYFTLFAAFSSYGAVGSLLAVFIALWVFNICLIIGLKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLIVDHAVLTKDLRRLVVGLVAFVVLFVVLSFSYRFGSRALMRAVNFESHALRVEVAD
HALKNLDPRNLVPGEVMSRSTADADSSTRIFGQIGTGVSAATGFLGAATYLLISDWLV
GLLVLVLVPIISGVVALASKGISKRSVTQQEKLAESGAQASDIMMGLRVIKAIGGERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVKTFEKASQASARAAVDTAVASGKVAGIGEISIAVNIAAVLLIAGWRYTTGELGPGQ
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complement (6781. .6987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB98345.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 328478 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCG 328419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGCGTCGGCGCGAATACGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transI table=11
/product="ABC-type multidrug/protein/lipid transport
gystem, ATPase component"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEISRAKQLQAGMPAEDYSLVPPRSIEKVAKMKQRQQRLMDQAAAIREESN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
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PF00664:ABC transporter transmembrane region."
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db_xref="GI:21323718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                         product="Hypothetical protein"
protein id="BAB98343.1"
db_xref="G1:21323717"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                  (1869.
                                                                                                                        complement (6781.
/gene="Cg10950"
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10107. .11843
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                                                                                                                                                                                                                                                                                                                                                                                         .8205
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Matches 873; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      7048.
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EREASLEVTERLEARGEDDELHOTLGGHLAAMSVKSELALALARGGDDELBELBELGE
LTRTSMSENROVESRYTVWILATE GGHELLADAHTHLSVIGTTSQVSPARFELCAM
LVREATTNILRHSDATDATLTLSSTEVRMDNNGVNKDIGRLSGLSALRSRAESAGMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTSTLEVIEGLSAPSSGTVRISGLDPVADRAILRPELGIMLQSGGLPSQLTVAETMDM
WHGTCTYPRAIKDVLADVDLLHRENVKVGALSGGEQRRLDLACALLGDPSILFLDEPT
TGLDPESRRHTWQLLLDLKQRGVTWMLTTHYLBEAEFICDRIAIMNAGEIAVEGTLDE
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CSALALMTSGFTRNARAQMTSMPVFWLAMGGLGSIRFVFGDSIVADILAYTPFAIS
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YTRVSLQAIPVVLLSAYFLGIVANAGTLNPSFVWLLGFSVILLIVTVLVYEYQPSLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVAREKSIISFVLRGGQVELPVLSGAEIIRDNNHVRIATTTLQQHTLEILTWAAETGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLVQIGWAGATFADSVGGVEAANFAGIFQDMLIPLGILAAWTAAAVWAANRYMRWDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPRRSVQPFFFTGLVLNVLGVVVSVVLQIPGLNMSDNTRATALIFTLTCVFLLSIAYI
                                                                                                                     IIGR01184:ntrCD: nitrate transport ATP-binding subunits
                                                                                                                                                                                              binding subunit
TIGRO1187:potA: spermidine/putrescine ABC transporter
ATP-Danding subunit
TIGRO1188:darrata daunorubicin resistance ABC transporter
ATP-binding subunit
ATP-binding subunit
/codon starta.
                                                                                                                                                                               TIGR01186:proV: glycine betaine/L-proline transport ATP
         TIGR00968:3a0106801: sulfate transport system permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="Two-component system, sensory transduction
                                                                  IIGR01166:cbiO: cobalt transport protein ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporter, permease components"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulators
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P00196:Bacterial regulatory proteins, luxR family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Two-component system, response regulators consisting of a CheY-like receiver domain and a HTH
                                                                                                                                                                                                                                                                                                                                                                                                                                            'producE="ABC-type transporter, ATPase component"
'protein id="BAB98339.1"
'db xref="G1:21323713"
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db_xref="GI:21323716"
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db_xref="G1:21323715"
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                                      100.0%; Score 873; DB 6; Similarity 100.0%; Pred. No. 4e-185; 73; Conservative 0; Mismatches 0;
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Sequence 3454 from Patent EP1108790.
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AX123538.1 GI:14041026
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/organism="Corynebacterium glutamicum"
/db.xrefe"taxon:1718"
/note="Seg 1 to long (3.309.400) split in 11, seg 7063
1.200.001 1.549.980"
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1 (bases 1 to 349980)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokod, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynucleotides
Patent: EP 1108790-A 7063 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LID. (JP)
Location/Qualifiers
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Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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Sequence 7063 from Patent EP1108790.
AX127147 AX114121
AX127147.1 GI:14041135.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCCTCCTCCCGCCATGAACTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGTACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCTCAGACAGGGACTTACCCTGGCTGGCGGGAACCCTCTGGAATTCCATCGAGATA
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                                                                      Corynebacterium.

1 (bases 1 to 627)

Nokagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.

Novel polynucleotides

Patent: EP 1108790-A 3454 20-JUN-2001;

KYOWA HAKKO KOGYO CO., LTD. (JP)

Location/Qualifiers
                                                                                                                                                                                                                                                                                            ;
0
                     Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                 Score 568; DB 6; Length 627;
Pred. No. 8.9e-117;
                                                                                                                                                                                                                                                                                                                     GTTTTCGCGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGT
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                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                    1. .627
/organism="Corynebacterium glutamicum"
/db_xref="taxon:1718"
159 c 185 g 144 t
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                                                                                                                                                                                                                                                                 65.1%; Score 568; DB
llarity 100.0%; Pred. No. 8.9
Conservative 0; Mismatches
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                                                                                                                                                                                                                          185 g
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                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 568;
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KEYWORDS
SOURCE
ORGANISM
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AX067087/c
LOCUS
                     SOURCE
ORGANISM
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ACCESSION
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ORIGIN
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                                                                                                      AUTHORS
                                                                                                                                            JOURNAL
                                                                                        REFERENCE
        KEYWORDS
                                                                                                                                                                      FEATURES
                                                                                                                               TITLE
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/db_xref="G1:125
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1 (pases 1 to 993)
Pompejus,M., Kroeger,B., Schroeder,H., Zelder,O. and Haberhauer,G.
corynebacterium glutamicum genes encoding proteins involved in
membrane synthesis and membrane transport
Patent: WO 0100805-A 669 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 AGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGCTCTGGACCG
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Pred. No. 4e-80;
0; Mismatches 3; Indels 2.
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    .993
/organism="Corynebacterium glutamicum"
/db_xref="taxon:1718"

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WO0100843.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/note="RXN03164"
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AX063771
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98.8%;
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/trānslation="MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLI
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FVFIGGVGGYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVV
192 c 246 g 217 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

1 (basea I to 708)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynucleotides
Patent: EP layon 3455 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%; Score 326; DB 6; Length 822; Best Local Similarity 100.0%; Pred. No. 1.3e-62; Matches 326; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                   /organism="Corynebacterium glutamicum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3455 from Patent EP1108790.
                     Patent: WO 0166573-A 51 13-SEP-2001;
BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
                                                                                                                                                                           /codon_start=1
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_173 c 221 g
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                                                                                                                                       101. .802
/note="RXA01394"
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SOURCE
ORGANISM
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ACCESSION
VERSION
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FVFIGGVGAQYGDTGRWIFAAGAFAASLIWPPLVGFGAAALSRPLSSPKVWRWINVVV
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                                                                     1 (bases 1 to 822)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. corynebacterium glutamicum genes encoding metabolic pathway
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1 (bases 1 to 822)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O., Haberhauer, G., Kim, J. W., Lee, H. S. and Hwang, B. J.
Corynebacterium glutamicum genes encoding metabolic pathway
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                     Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Corynebacterineae, Corynebacteriaceae,
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100.0%; Pred. No. 1.3e-62;
tive 0; Mismatches 0; Indels
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    822
/organism="Corynebacterium glutamicum"
(db_xref="taxon:1718"

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Corynebacterium glutamicum
Bacteria, Firmicutes; Actinobacteria;
                                                                                                                                               Patent: WO 0100843-A 53 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
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AX244059
                                                                                                                                                                                         Location/Qualifiers
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   Corynebacterium glutamicum
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Matches 326; Conservative
                                                       Corynebacterium.
                                                                                                                                   proteins
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AUTHORS
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Gaps 9

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TDAVVDAARAGLRT"
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Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti
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Phyllobacteriaceae; Mesorhizobium.
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Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1620 ATAGGTGTGGCGGTGCTCACCGGATTGGCCGTGAAGCTGATCCTGATGGGTTA 1675
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345763 bp DNA linear BK
Mescrhizobium loti DNA, complete genome, section 8/21
AP003001 BA000012
AP003001.2 GI:14023393
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Mesorhizobium loti
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                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                           /gene="lysE"
981. .1676
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Best Local Similarity 78.4%;
Matches 232; Conservative
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FPPVFAEVAHWGAVTLTLRVEDBAHTLSLLRRGSVLGAVTREADPVAGCEVLRLGVMR
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lysG, lysE of Corynebacterium efficiens
Published Only in Database (2002)
2 (bases 1 to 1771)
Itaya, H., Kimura, E., Kawahara, Y. and Sugimoto, S.

Direct Subnission
Submitted (04-APR-2002) Hiroshi Itaya, AJINOMOTO CO., INC,
Permentation & Biotechnology Laboratories; 1-1, Suzuki-Cho,
Rawasaki, Kawasaki, Kanagawa 210-8681, Japan
(E-mail:hiroshi itaya@ajinomoto.com, Tel:81-44-244-7123(ex.4146),
Fax:81-44-222-0129)
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/db_xref="taxon:152794"
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Pred. No. 1.8e-57;
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AVATHICYNRERDIIAKIPOVDVVGGHSHTLLLANDPRAAGSYPTPWUNDRGGYKVPVV
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VAPMERULTULPRONTLATFQISGUDLONAGLESGLGJEDGGARPPOVAGLKYSPDKS
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GLEOVVADYLGAARREYTFKLDGRITTEIAATVAAAPAAEPAKPAEATPAPAPAQGPPKFA
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ITTYATATANDOLFRALMKLRARAIRSVPPYTARLASSIERHLATLDFESPEVV
DKTVBEKLGKOGVKSIAIVNPGFSVVOLIETLDEIGREAAETFHHAGGKNFAHIPCLNDS
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GEAVVATKDGPTITARHVVLATGYELVDIVPAAAHRIISTWAIATCPQPRKLWPGPAF
IWEASDPYLYLRATADGRVICGGEDEDFADETRRDELIADKSARIADKLGRLFPYLDV
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GTVEEEFLNOMKPDAVTLGNHEFDDGESALVPYLDKAKFPIVSANVMPNDKSGAAGKI
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IYEANKGQRPHRLTPGATLTIPAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
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/db_xref="GI:14023401"
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/gene="mlr3019"
6381. .7442
/gene="mlr3019"
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/gene="mlr3020"
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/gene="mlr3020"
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/gene="mlr3021"
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/transl_table=:
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/transl_table=
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Grellsktyregis ptoaglestyregarkayderdderbernaalfoller ig tosyte
Grellyvperlkreddhpellyvevanddrivdig leberodder is togerstaa
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AIDTLTLSLSRELGARNIRVNIVAPGYTHTEMTEGMVGTDFGNMLIAGVPLGQRFGKF
DDIAPTVAFLASDEAAMLTGERINASGGAR"
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SRMTVLDPRDTDRKLLDBRGTAFVQBAVTENNYKKLLTPLLTNGGGGGFCVNLSVDTG
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YLEQPGANTRVRSWCPTPGAQYGLLVTHNEAISIADFFTVRSKGKKVYYRPTCHYAXH
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AEARKLAPYQNATGMQVTSAVLAGMVWALENPDAGIVEADEMDYKRCLDVQSPYLGPV
KGYYTDWTPLDRRPGLFPEDLDRSDPWQFRNILVR"
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TVATDTGGKLADGSYTWTGATSVEINGTSLIRQTPVSFNCLLISTSQLNCTSSSGQNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="short chain dehydrogenase or 3-ketoacyl-CoA
URL:http://www.kazusa.or.jp/rhizobase/,
Tel:81-438-52-3335 (ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced gi:11994976.
Location/Qualifiers
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/strain="MAPF303099"
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complement(6. 884)
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/gene="mlr3013"
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/gene="mlr3014"
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/gene="mlr3016"
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'gene="mlr3017"
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/gene="mlr3017"
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trans table=
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/transl_table=
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TVVELEDAKGLEKLPFRKGGPFEAHDDGEGGHEAHAGHTEDBGAHDHGNDHAGSEEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGAYDTHLWLDPANAKAMAQAIETALIAADAGNAATYQANTKKLIDDLDALDAEVVET
VKPVKDKPFIVFHDAYQYFEHRYGVKTAGSITVSPETLPGADRVKQMQEKVRQLGAPC
VFAEPQFEPKLVSVITEGTAAKSATLDPEAATLIPPGPDLYFKLMRGIAGSLKNCLS"
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                                               8472 bp DNA linear BCT 18-DEC-2001
18 str. C58 circular chromosome, section 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FGITEVLSTTQYHLVVTPHIHAKDSMVPIRYILETGSADGVIISKIEPNDPRVRFMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDAPDIGAETKERVRLIARQIGYQPNRAGVRLRTGKTNVIALVLSVDEELMGFTS(
                                                                                                                                                                                          Agrobacterium tumefaciens str. C58 (Cereon).
Agrobacterium tumefaciens str. C58 (Cereon).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Cereon) "
                                                                                                                                                                                                                                                                                            1 (bases 1 to 8472)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 8472)
Hinkle,G., Slater,S.C. and Goodner,B.
Direct Submission
Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
Location/Qualifiers
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/note="(AE005408) putative adhesin"
/codon_start=1
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2640. .5138
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                                                                      Agrobacterium tumefaciens str. Ct
of 254 of the complete sequence.
AE008076 AE007869
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                                                                                                                                                 GI:15156608
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                 AE008076.1
                                                    AE008076
                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
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  RESULT 12
AE008076/c
                                                  LOCUS
DEFINITION
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
                                                                                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ACPHGLAPTTSTLLQLVIGDALAIALLEARGFTPDHFRTFHPGGQLGANLTMVSEIMR
VGDQMPLAVLGTKMPEAVMTLSQKKVGCVLIVDANGELAGIITDGDVARNLHRNLADV
                                                                                                                                                                                                                                                                                                                                                                                           PFAQAVDMISKIEGRLIVTGVGKSGHIGSKIAATLASTGTPAFFVHPVEANHGDLGMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVDEVMTRTPKTVDPQTLAGTAIALLNEHNIGALVVTRNNMPLGVVHFHDLLRIGAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 249436 CGATCTCGGCCAATTCGGCATCGCTGAAGTCGAGCACCTTCAGGGCGCCGACGCAGTCCT 249495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 249496 CGACCTGCTCCGGCCGGCTGGCGCCGATCAGCGCCGACGTCACCTTACC----- 249544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGCAGGCCCTGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 CGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCTCAT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CTTGCGCAGCCAGGCCAGGCCATCTGCGCCAGCGTCTGGCGGCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 CTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGAAGTGACTGCCCGCGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 ACAGGGACTTACCCTGGCTGGCGCGGGAACCCTCTGGAATTCCATCGAGATATTTGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249658 TCAGCGACTTGCCCTGCGAGGCACGGCTGCCTTCGGGGATGCCGCCAAGATATTTGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTGGCTGATGAATCAGAAGCGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 CCAGCTGCTCAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 345783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 141.2; DB 1;
Pred. No. 2.5e-21;
0; Mismatches 208;
                                                                                                                                                                                                                                            'note="hypothetical protein"
                                                                                                                                                                                          complement (10629. .11630)
                                                                                                                                                 complement (10629. .11630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unknown protein" / codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1830. .13626
gene="mlr3024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="mlr3024"
                                                                                                                                                                             /gene="mll3023"
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ilarity 57.0%;
Conservative
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Best Local Simi:
Matches 319; (
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TTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTA

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445 ACTGACGAAGCACCAATCCACTGGTCACGGTATCCGCGCGCCGTACTCTCCTTGCTCG

385 AACTCGCCGTCAGAAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCTCA

564

CGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCA 6101 dechenacionaria de la reconstrucción de la contracta de l

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TGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAACAAG

5921 récéccaécéasaaasacarcarecearacearacearrecreesegrar-----

5981 CTCTGTGAGGCACGGCTGCCATCCGGCACACCCAGATATTTCGTCGTCAGCATGCCC

CCCTGGCTGGCGCGGGAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGCAGCCCC

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745 ITCTCACCGTCATCGCCCGGTTCCTCCAACGATTAATGATGAATAGCTTGGCTGA

5869 -----caacaagaccercricercearceacecricarcearcearaecerce

5816 TGGATGATGCAGGGCGTGCCGAGATCCTTCAGAATAGCGGCGCCTCGCGGGGGCGCTTC 5757

805 TGAATCAGAAGCGGCGGCGCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGCTCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISAKYNDDPCVAWLGNDGAGHFVKTIHNGIEYADMQMIAEITGIETGIEGEKWSYNEID
VPAERNKGRLNSYLIEITEKVLRAADPITGKPWYDLILDKAGGKGTGKWSYIEAQNMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MKYNHCGKTGLKLPAISLGLWHNFGNDTPHQTKQAICRRAFDLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THPDLANNYGPPPGSAETAFGEILKTDFRGYRDEMIISSKAGYNMWPGPYGEMGSRK
YLISSCDQSLKRMGLDYVDIFYSHRFDPNTPLEETCGALDQIVRSGKALYVGISSYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MEQAEIGLIGLGVMGSNLALNIAEKGNKIAVFNRTPEVTRKFYA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAGELQGQIIPCETIEEFVAAIRPPRPIIIMIKAGDPVDQQMEILKPHLANGDIMIDA
GNANFRDTIRRFDNLKDSGLTFIGMGVSGGEEGARHGPSIMVGGTEDSWKRVEKVLTS
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                                                                                                                                                                                                                                                                                                                                                     C_2811"
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6465. .6791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain K-12)"
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Agrobacterium tumefaciens str. C58 (U. Washington).

Bacteria, Protebacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.

I (bases 1 to 13051)

Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K.; Almeida Jr.,N.F.,
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G.,
Callet,W., Grant,C., Guenthner,D., Kutyavin,T., Levy,R., Li,M.,
McClelland,B., Palmierit,A., Raymond,C., Rouse,G.,
Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I.,
Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M.,
Krespan,W., Perry,M., Gordon,D., Eisen,J.A., Funderick,C.,
and Nester,B.W.
Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
The genome of the natural genetic engineer Agrobacterium
                                                      BCT 20-DEC-2001
                        Agrobacterium tumefaciens strain C58 circular act 20-DBC-200 137 of 256 of the complete sequence.
AE009111 AE008688
AE009111.1 GI:17739946
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Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
Wood, D.W., Setubal, J.C., Kaul, R., Mora, V.K., Almeda Jr., N.F.,
Zhou, Y., Bovee, Sr., D., Chapman, P., Clendenning, J., Deatherage, G.,
Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M.,
McClelland, B., Palmieri, A., Raymond, C., Rouse, G.,
Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumefaciens C58
Science 294 (5550), 2317-2323 (2001)
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RESULT 13
AE009111/c
                                                                            DEFINITION
                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                ACCESSION
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AUTHORS
                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                     REFERENCE
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Pred. No. 3e-20;
0; Mismatches 204;
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15.6%; 56.8%;

Best Local Similarity 56.8 Matches 312; Conservative

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Query Match

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FEATURES

CDS

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KOAICRRAPDLGITHFDLANNYGPPPGSAETAFGELLKTDFRGYRDEMIISSKAGYNM WPGPYGEWGSRKYLISSCDOSLKRAGLDYDD IYSERFDPRTPLEETCGALDQIVRSG KALVYGISSYNSKRTREAAALLKULGTPCIIHQPSYSMINRWIEBDGLVDTLEELGIG SIVESPLAGGMLTTYKTGAPDGSRASOSKSINPAELNERNYENIRALNSIAERRGYT LAQMAIAWVIRGGRITSALIGASRVEQVEDCVKALDNAEFSTEELAEIDRYAKDADIN
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FGAHGFERTDGVDKPHGPWGSGADIF"
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   RDFENFVYLSQVQQALAIRTAVDYWRSLKPHCMGTLYWQLNDTWPVASWSSLDYGGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'trans<u>T</u> table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MVWQPAENRYASMKYNHCGKTGLKLPAISLGLWHNFGNDTPHQ1"
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coated using Blastx/Glimmer"
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BEHRHDEDRBARAYERVERLAGCGRKRIAVIVPSRRSFRBHDHARGFROGINDE
PPIDAVTIETPLEKIRFGRGLAGSBRPDGIVSISGSSTIALVAGFRAAGVKIGEDV
DIVSKQSAEFLAWIKPQIHTVNEDIKLAGRELAKALLARINGEAAETLQSISGEVWSS
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REKTEDLLCSAVBANMINI I RVWGGGFYEEDWFYDLCDRLGLLVWQDFMFACNLYPCSE
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Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
Karepan, W., Perry, M., Gordon. Kamm, B., Liao, L., Kim, S., Hendrick, C.,
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and Nester, E.W.
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                                                                                                                                Direct Submission
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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identified by sequence similarity; putative; ORF
coated using Blastx/Glimmer"
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located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                      /organism="Agrobacterium tumefaciens str. C58
Washington)"
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transl_table=
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gene="manA"
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CDS

CDS

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Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
inttp://www.nih.go.jp/
inttp://www.nih.go.jp/
inttg://www.nih.go.jp/
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inttg://ww.nih.go.jp/
inttg://ww.nih.go.jp/
correct initiation codon. Where possible we choose an initiation codon (arg., tgg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 7H9 Lies between and overlaps with cosmids 5F1 and 2H2 on the AseI-A genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also included but some or concording the state of is given for codons is given for codons is given for CDS.

Usually the highest scoring match found by fasta or is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Processes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
Submitted (16-NOV-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich, Research Park, Colney, Norwich, Norfolk WR4 7UH, UK On May 9, 2002 this sequence version replaced gi:11228487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="nominal overlap with Streptomyces coelicolor cosmid St7H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (583. .618)
/note="possible stem loop. Score 51: 17/17 (100%) matches, 0 gaps"
                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (URL, http://www.sanger.ac.uk/Projects/S coelicolor/) CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
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alanyl tRNA synthetase; amidase; integral membrane transport
protein; katA2, catalase; oxidoreductase; regulatory protein;
tetR-family transcriptional regulator; transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                     Redenbach, M., Kieser, H.M., Denapaite, D., Bichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nominal overlap with Streptomyces coelicolor cosmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Streptomyces
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                                                                                                                                                  Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 15586)
Seeger, K.J. and Harris, D.
Unpublished
3 (bases 1 to 15586)
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FDATVSLLFFLLIGKTLDHIMRDKARSAIAGLARLSPRGATVIDADGVRDYRPLADIE
PGMSIAIAAGDRVAVDAVVCGSSDLDMSIVNGESAPRRVVAGDSLQAGTLNLIGSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARVTASAKOS FLSEVI GLMEAAEGGRARYRRI ADRAASYYS PVVHLLÂLVTFLGWGTF
GODKOAMLTA TAVLI ITTOCLLGLAVEVVQVYAAGRLLERGETINKEGSBAMERLISEID
TVLEPKTGTLTVGREKLUFTDVKPA IMA TAGLAAHSKHPISKALHAAYNGALPAYE
AVREI PGSGVEAETEAGTYRLGNRRFACPDETRI NNGDARSEVVLSLIDGRHLASFGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MSCCAPGTEGSLELGEPLNPPSSEELLLASRDLGQGLRQTDLSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVYCGACITTIETALGRLGQVERARVNLSSKRVAVVWKEEVNGVRTDPADIARAILA
TGYRIHLFASGQDASYALRSQLIRAVALCGFASANIMLLSVSVWSGADAATRDMFHWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ~
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                                                                                                                                                                                     note="identified by sequence similarity; putative; ORF
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                                                                                                                                                                                                                                                                                /codon_start=1
/transi_table=1.
/product="nitrogen fixation protein FixI"
/protein_id="AAL42533.1"
/db_xref="GI:17739594"
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Pred. No. 2.9e-20;
0; Mismatches 204;
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AL450223 AL645882
AL450223.2 GI:20520842
                                             /note="Atu1528"
complement(8593. .10884)
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Best Local Simi
Matches 312;
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gene

CDS

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/codon start=1
/transI_table=11
/product="conserved hypothetical protein"
/protein_id="CAC16513.1"
/db_xref="GI:11228491"
/db_xref="STREMBL:09EWJ2"
/db_xref="STREMBL:09EWJ2"
/db_xref="MIVITAPTGNIGRRILPLILESAPARGEELRVIVRDPARLAAPV
RENYEVYTGSHGDPAYVDRAFDGADAVFWIVPPDSSRTPDDAYRGFTRPAAHALVAHG
VGHVVGVSALGRGTPVAARAGLVTASLAVDDLIAETGVAHRALASPSFFENLLEEADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMEL:Q9EWJ1"
/translation="MPERTAHTPVTARMLVXTTPEWLALTVEERVHAFTTEVVPVVRA
RTAGVRSRFYDTEFYSARVTDVWVWEADDHHAYQLLVDALRETPFWDRYFEVVDLLVG
TENGYARTYGVDAVTTLST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IREHGCFTDVLDADRKSPLVAVADIASVAAGLLLDRSWTGTGSVPVLGPRDLSPNDLA
RIMTERLGRPVRYERHTLDDLRSTLVGYGLDKDFVDGVVDMKRAKDDGLDAGVTRTPD
                                                                                                                                                                                                                                                                                                          gene="SC7H9.03c"
note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3711. .4604
/gene="SC7H9.04"
/notes="SC7H9.04, hypothetical protein, len: 297 aa;
similar to TR:Q9RCY4 (EMBL:AL133469) Streptomyces
coelicolor hypothetical 31.4 kDa protein SCM10.14c, 299
aa; fasta scores: opt: 791 z-score: 890.7 E(): 0; 46.4$
       transcription activator carboxyl terminal region, score 37.90, E-value 3.9e-10" complement (3134. .3562) /gene="SC7H9.03c"
                                                                                                                                                     /note="Pfam match to entry PF00126 HTH_1, Bacterial regulatory helix-turn-helix protein, lysR family, score 61.20, B-value 1.7e-14"
complement(3428 .3520)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6218 CCGTCGACGACCGCGTACTCGTCGATCTCGGCCAGTTCGTCGTCGTCGAGGACGGGTTG 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 ITCACGITCAACAIGCCCTCAGACAGGGACTTACCCTGGCTGGCGCGGGAACCCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 GCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6158 gccadadegedeacerrerecrecadergerregecegeagedaceaecagearea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 CCGGCGTCGTGGGAAATCTCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 GTCACGGTATCCGCGCCGTACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCCATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein SC7H9.05"
[protein_id="CAC16514.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aa "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="SC7H9.05, unknown, len: 121
codon start=1
transI table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.3%; Score 133.6; DB 1;
Best Local Similarity 57.5%; Pred. No. 1.4e-19;
Matches 300; Conservative 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dentity in 302 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:11228492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATPTTFEDWVARTLGPVVLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4688. .5053
/gene="SC7H9.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            688. .5053
gene="SC7H9.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="SC7H9.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SC07592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="SC07593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1679. .4682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4604
                                                                                                                                                                                                                                                                                                                                                                                        signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1688.
                                                                                          misc_feature
                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RBS
                                                                                                                                                                                                                                                                                                                                                                                                                               RBS
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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complement (641. .2161)
/gene="SC7H9.02c"
/note="SC7H9.02c"
complement (641. .2161)
/gene="SC7H9.02c"
complement (641. .2161)
/gene="SC7H9.02c, katA2.
complement (641. .2161)
/gene="SC7H9.02c, katA2, catalase, len: 487 aa; similar to SW:CATA MICLU (PIR:S27264) Micrococcus luteus catalase (EC 1.11.1.6) KatA, 497 aa; fasta scores: opt: 1791 z-score: 2040.9 E(): 0; 54.8% identity in 484 aa overlap and to SW:CATA STRCO (EMBL:AL035478) Streptomyces coelicolor catalase KatA or SC365.25c, 487 aa; fasta scores: opt: 1699 z-score: 1936.3 E(): 0; 53.8% identity in 483 aa overlap. Contains Pfam match to entry PF00199 catalase, Catalase and matches to Prosite entries PS00438 Catalase proximal active site signature and PS00437 Catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (2636. .3598)
/gene="SCTH9.03c"
/note="SCTH9.03c"
/note="SCTH9.04c"
/note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDPETRVEELVTLRWTAAVRPCHPLTEGPLTAARFAAAEHVGVSRRGRPDGPVDAALA
EHGLSRRVSVVLPGHLAALSLAARTDVVALVPAARDEADFSPSPLTEQARVLGLCLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTDTPPATTTDSGAPAESDEHSLTAGPAGPVLLQDAYL.IEQMAQ
FNRERIPERQPHAKGSGAFGHFEVTHDVSAYTKAAVFQPGTRTDLVARFSTVAGERGS
PDTWRDPRGFAVKFYTSQGNYDMVGNNTPVFFVKDPWKFQHFIRSQKRRADSNLRDHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQMDFWTLSPESAHQVTWLMGDRGIPRTWRHMNGYTSHTYMWINASGERFWVKYHFKT
DQGIBYFTQHRADQMAAADTDYHMRDLFEHIRDGDFPSWTLHVQVMPYEBAAGYRFNP
FDLTKVWPHGDYPLIPVGRWTLERNPTDNHAEIEQAAFQPNNLVPGIGPSPDRMLLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFSYADAHRYRIGANYQQLPVMAPVVDVRTYSKOĞAMAYRKTTDPVYAPNSKGGPAAD
TEHFGTPPSWETDGSITRTAYVSHAEDDDWGQPGTLVREVMDDAARDRLVDNVVDHLL
NEVTEPVLQRAFAYWSNIDRTIGDRIAKGVRAKAGEKDFKAAEQRNPARQAMQDKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnstdptapv1danlavaldallaegsytraaarmrtspaamsr
Tlgrlrrllgdplllvraggtwvptpralalrdeaatvyrrlgalltpatgydpatlrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFSLQTADLVGAALAAGLLTLAGQEAPGVSLRFRAEELEAGPALRDGRVDLEVGAIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF00199 catalase, Catalase, Score 925.90, E-value 1.1e-274"

complement (1136...1162)
/gene="SC7H9.02c"
/forte="PS00437 Catalase proximal heme-ligand signature"
complement (1979...2029)
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/gene="SC7H9.03c"
/note="Pfam match to entry PF01046 NodD_C_term, NodD
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complement(2636. .3598)
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db xref="G1:11228490"
db_xref="SPTREMBL:Q9EWJ3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               table=11
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trans1 table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1/transl_table=
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Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
Prantes, Laboratoire de Genetique et Developpement UMR6061-CNRS,
Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
France, GATC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany,
Universitaet Bielefeld, Biologie IV (Genetik) Universitaet stelefeld, Germany, Unite de Blochimie physiologique,
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20,
B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
des Sciences Agronomiques de Gembloux, Avenue Marrechal Juin 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
:ed (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear BCT 05-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.

(bases 1 to 306250)

Capela, D., Barloy-Hubler, F., Gouzy, J., Bothe, G.; Ampe, F., Batut, J.,
Boistard, P., Backer, A., Boutry, M., Cadieu, E., Dreano, S., Gloux, S.,
Godrie, T., Goffeau, A., Kahn, D., Kiss, E., Lelaure, Y., Masuy, D.,
Pohl, T., Portetalle, D., Puehler, A., Purnelle, B., Ramsperger, U.,
Renard, C., Thebault, P., Vandenbol, M., Weidner, S. and Galibert, F.
Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium mellioti strain 1021

Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
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                                                                                                                                                                                                                 B-5030 Gembloux, Belgium. B-mail:Jerome.Gouzy@toulouse.inra.fr
http://sequence.toulouse.inra.fr/meliloti.html.
Location/Qualifiers
5996 TCGTCGGTGAGCCAGCCGGTCGCGAAGGACTTGCCCTGGGTGGCGCGGGGACCCCTCGGGC 5937
                                                                                                5936 ACGCCCTCGAGATAGCGGCCGCTGAGCAGCCCCTGGGCCAGCGGGTGAACCCGATGAACG 5877
                                                                                                                                                                                                                                                                                                                                5831 Arccaccigaricadcardraciacacddcrideriddarcadddgraeddccagarca 5772
                                                                711
                                                                                                                                                                                                                                                                              772 ACCCAACGATTAATGATGGAATAGCTTGGTGATGAATCAGAAGCGGGCAGCCCTCCTCC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sinorhizobium meliloti 1021 complete chromosome; segment 7/12.
ALS91788 ALS91688
ALS91788.1 GI:15074579
                                                       652 ATTCCATCGAGATATTTGTCCGTGAGCAGGCCCTGCGCAAGTGGTGAGAAAGCAATGACG
                                                                                                                                                                712 CCAAGACCATTGTTGGCAGCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                              5771 cgcagcarceccecececececececececerceres 5730
                                                                                                                                                                                                                                                                                                                                                                                          832 GCCATGAACTCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 873
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488. .2707
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Sinorhizobium meliloti
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MELILO EU Consortium:
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SME591788
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VERSION
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AUTHORS
TITLE
JOURNAL
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PUBMED
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SOURCE
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KDWADKYKGKFDDGWDAMRERIYARQKQLGWIPQUTPRPDTLSGWEDIPEDEKPP
RELMEVPENGATYEHADVOGARLLEALDELGIRDNTLIFYVENDNGSSARGONGTISEL
LAQNOI ETREIKDHIRAMELGRADULGSPKADNMYHAGWAMAGSTPHRSTKLVAAHFG
GTRTFLVVSWPGKIKPDGTPRSQFHHLNDIVPTIYDVLDIQPPKLYDGISQDELDGVS
BYTTPDSPEASGQKRQYFEINGSSRYTYDBWATASVFGPRIPTRYAGLDAPIFKWRSDDN
DLWELHDLSQDYSQARQVARADHPEKVBALKARAFGYQARANKYPPVGGGLWSAYPHPED
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VENIVRVDPSHGKEGYHFTEDMINKAVTWMKQVHAALPDRFPFWYWAPGAAHGPHIF
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KRINWILABDYDVDVOYGSQLADMGRQRPRFTLFVSRDDRALAVSRRWGNVSRLGAI
DPBQSPYKBELAAUTTVUDLFKI KRADNLHPTKAESPEI VRLIGSRLSSGOTLTDS
RLGLGDHI VAATAGAAHTVGTAAGLVVAAPAAI VDQWTRRNYVHHVEALAEPSGARR
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KEVAKGHVPRSAPLAFTANDAFDVGKDSYSPVALAYFDRKPFAFNGKI ESLKVEYLK'
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LNTHVRKSPDGSVLVFIHGFNNHFEDAVFRFAQIIHDSGARSVPVLATWPSRGSLLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MLLYGCAGRPTGVLEPVAANPSAAQVEMLVTTTRSRAEKPGEMF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2887. .4062
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/function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
predicted by Codon usage
predicted by FrameD"
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degradation; degradation of dna"
/note="Product confidence; probable
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(db_xref="GI:15074580"
(db_xref="SPTEMBL:092PT4"
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/transl_table=11
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Gene name confidence : hypothetical
predicted by Codon usage
predicted by FrameD"
/codon start=1
/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'function="miscellaneous; unknown"
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/gene="xthA1 OR SMc00956"
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|gene="xthA1 OR SMc00956"
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predicted by Homology
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(db_xref="G1:1507888"
(db_xref="G1:15078881:059289"
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                                                                                                                                                                                                                                                                                  KA I EAAGYGA I WHGQKSWNGVA I LARDREPTLTRKGLPGDPDDTHSRY I EAAVEGWY I
GCLYLPNGNPYPGPKFEYKLAWFHRLTAYAAELLELDVPVI LAGDYNVMPTELDVYKP
                                                                                                                                                                                                                                                                                                                                              ERWVNDALFRIEVRDAYHRLLEQGWTDALRQLHPGERVYTFWDYFRNAFARDAGLRID
HLLLSPHVTLRLSAAGVDRHVRGWEHTSDHAPAWIELSDGPAEEDQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IILSDGGKVADLEQVLGFVAPDIPVLTLPGWDCLPYDRVSPSADTSARRLAALSALIA
HRKPHPAIVLVTINAALQRISPQDVIESLAFTARPGNQIRMDDLAARLERNGFERVP
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SLITTPPVDRMAVRTFISPPDALVIRETLMREHYRGGQSFYVCPRVSDLPEIHDFLKS
                                                                                                                                                                                                                                                    translation="MKIATYNVNGVNGRLGVLLRWLEEASPDVVCLQELKAPDPKFPV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAVRGGILDVYVPGSGEPLRLDPFGDTLEAIRSFDPASORTIGOVRSLDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DETEDQLNSIDAVRDDLGRGRPMDRLVCGDVGFGKTEVALRAAFIAAMNGVQVAVVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYLTAKGFGEALNDLNAVRLSPFTEHEGEARQVVNI EARQGLRWAKPAGEADNDGTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evidence=not experimental
trans1 tab1e=11
product="PROBABLE TRANSCRIPTION-REPAIR COUPLING FACTOR
                                                                                                                       product="PROBABLE EXODEOXYRIBONUCLEASE III PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macromolecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Product confidence : hypothetical sene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="HYPOTHETICAL/UNKNOWN PROTEIN"
protein_id="CAC46229.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not experimental
complement (6137. .952)
/gene="mid OR SMc04450"
complement (6137. .952)
/gene="mid OR SMc04450"
/function="macromolecule metabolism;
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tene name confidence : probable
predicted by Codon usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="miscellaneous; unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYERDPDPADDISEQVIEEPSNNWPAAD
                          'codon_start=1
'evidence=not_experimental
'transl_table=11
                                                                                                                                                                                                                db_xref="SPTREMBL:Q92PT1"
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transl table=11
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restr./modif."
                                                                                                                                                    /protein_id="CAC46228.1"
/db_xref="GI:15074583"
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predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="SMc00958"
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Search completed: April 26, 2003, 23:44:41 Job time : 3110.77 secs

DVPELKVAVAHGOMPATELEDIMNAFYEGRYDVLLSTTIVESGLDVPTANTLIVHRAD MFGLAQLYQLRGRVGRSKVRAFALFTLPVNKTLTGPAERRLKVLQSLDTLGAGFQLAS

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HDLDIRGAGNILGEEQSGHIKEVGFELYQQMLEEAVAELKGEEEIHDTGWSPQISVGT
PVMIPEEYVPDI.NLRLGLYRRLGELTDLKEIDGFGAELIDRFGPLPTEVQHLLKIVYV
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                                                                  Score 115; DB 1; Length 306250; Pred. No. 1.8e-15;
                                                                                                             0; Mismatches 235; Indels
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                                                                                       Best Local Similarity 53.6
Matches 309; Conservative
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Sequence:

Run 'on:

Searched:

Database

Result No.

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AL077673 Drosophil
AL059317 Drosophil
AL099317 Drosophil
BE022218 894008G12
BQ818660 1030072D0
AL181962 Tetracdon
AL151258 Anopheles
AY108197 Zea mays
BB576857 BB576857
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AW190228 x160e6.x
BISBS15 DOC2BIJ O
BQ579715 WHE0308 H
BH614411 IC22HF7-T
BH843100 TC3-54P23
BH614228 IC22/2BB
AW015929 UI-H-BIOP
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BIG83498 464907 MA
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A1401605 tf60b01.x
A1820014 wj60d07.x
BG806166 2021-07 M
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                                                                                                                                                                                                                                                                                                                                                                   AW659102 96030 MAR
AL050923 Drosophil
BI724148 1031069C0
                    AI418751 tg33a02.x
AA452858 zx41c05.8
W91005 mf83h05.rl
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BI868875 603394947
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AA149286 z125e05.s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Salmonella typhimurium
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                              BI328066
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    .860
    .92ganism="Salmonella typhimurium"
/strain="LT2"
/db_xref="taxon:602"

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Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifscl.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                  BE025218
BQ818660
CNS026XT
CNS01MQH
AX108197
BB576857
AA150978
CNS01HIJ
AM190228
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AW659102
CNS007WH
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BQ578715
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BG048617
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Location/Qualifiers
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AF075981.1 GI:3320851
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AL108460 Drosophil
AL247708 Tetracdon
BH770958 LLMGtag68
BM712036 UI-E-DW1-
                                                                       April 26, 2003, 20:02:03; Search time 1163.26 Seconds (without alignments) 12154.292 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                  32308132
        GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                       US-09-105-117K-1_COPY_1421_2293
873
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                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Query Match
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Matches 47; Conserv
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence SP6 end of BAC BACN3108 of DrosBAC library from Drosophila melanogaster (fruit \{1y\}, genomic survey sequence. AL108460
/clone="390-T3"
/clone lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
sequencer"
                                                                                                                                                                                                                                                                                                                                                                        222
                                                                                                                                                                                                                                                                                                                                          681
                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGCGCAAGTGGTGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAAC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                         221 cccccccaccaccacaaaaccaaracraccaccarritriccrecaacaccccacacacc
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                                                                                                                                                                                               505 GGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCA 564
                                                                                                                                                                                                                                 400 CGCAGCATCCAGGCGAGCGCCATTTGATACAATTTTTGACCCCGTCGCGCAGCCAGTTCA 341
                                                                                                                                                                                                                                                                    TTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTA 624
                                                                                                                                                                                                                                                                                                Trcaacceceactrrrrccaerrrercececeraarcrerrerraaceaaaacee 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGC 861
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Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                        CCCTGCCTG----GCGCGGGAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742 AAGTICICACCGICAICGCCCGGIICCICCACCCAACGAITAAIGAIGGAAIAGCIIGGC
                                                                                                                                                             22;
                                                                                                                                 Length 860;
                                                                                                                                                               Indels
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/db_xref="taxon:7227"
/clone="BACN37L08"
                                                                                                                           Score 56.4; DB 17;
Pred. No. 0.00012;
0; Mismatches 151;
                                                                              207 t
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                                                                                                                             Query Match
Best Local Similarity 53.5%;
Matches 199; Conservative
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SOURCE
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LOCUS
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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1 (bases 1 to 664)

1 (bases 1 to 664)

1 (bases 1 to 864)

1 Sammes, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Barnot, A., Fizames, C., Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS03K4J linear GSS 17-MAY-;
Tetraodon nigroviridis genome survey sequence T7 end of clone
032B06 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          839 TSGSTBTSTBMSKBSSTSSTSBTSGSSBCGGSCGSTSGSSCSSBCGKSTSSGSTSGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019 SSTSBBTBTSTSSSSTTTTTTTTTTTTTTTTSBBSBBSSSSSTSSBBTSKSBTSBSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 CGGCGCAGCAGCATTGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTGGATCAACGT
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                                                                                                                                                                                                                                                                                                                                               Length 1101;
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                                                                                                                                                                             359 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 14.5%; Pred. No. 0.018; 47; Conservative 156; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                             u
                                                                                                                                                                             152
                                                                                                                                                                                                                                                                                                                                               Score 48.8;
Pred. No. 0.
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
a 176 c 160 g 1
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Tetraodon nigroviridis
Tetraodon nigroviridis
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FEATURES

7

2132

564

504

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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
751: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Parrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following respetitive elements were found in this CDNA
sequence: 143-166, >GC rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stāge="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 558)

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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                             1956 AATTCTTCGTCAGTAAATTCCAGACGTTCTAAAGCTGCAACATTTTCAATGATTTGTTGC 2015
                                                                                                                                                                                                                  2016 GGACGACTTGCCCCCAATCAAAGCTGATGTAACAGCTTTGAACTTTGCCCAGCTCTT---TCC 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2193 TAATGAGGATCACGCATTCGCGAATTTCAGGAATTCCATGCAAATATTTTCCTGTTAAG 2252
                                                             Gaps
                                                                                                                                                                                                                                                                                                               2073 CGTAAAACCCAAGCTTATGCCATTTGAGCTAGAGATTGTCCACGACTTTGAGCTAAATCA
                                                                                                  385 AACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCTCA
                                                                                                                                                                                         445 ACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCGTACTCTCCTTGCTCG
                                                                                                                                                                                                                                                                                                                                                                  565 TTGAGCTTGCGGACCATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 CCCTGGCTGGCGCGG-----GAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM712036
UI-E-DW1-ahc-g-16-0-UI.rI UI-E-DW1 Homo sapiens cDNA clone
UI-E-DW1-ahc-g-16-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                             505 GGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGGGGTTCCTGGGCGATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                           2133 TTAAGGGCTTGAACTTGTTCCAATCTTTCTGTGGTAAGACTGTCATGCAAAGTCGCA
                                                           6
                  Length 3237;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2253 AGTCCTTGATACAAAGGCTTAAAGGCAATTGTTCCTATCCC 2293
             Score 43.8; DB 17;
Pred. No. 0.82;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="UI-E-DW1-ahc-g-16-0-UI"
/clone_lib="UI-E-DW1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 AGGCCCTGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .558
/organism="Homo sapiens"
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               5.0%;
             Query Match
Best Local Similarity 49.9
Matches 170; Conservative
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BM712036.1
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BM712036/c
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                                                                                                                  : COBG032DA03LP1~end : T7"
8 others
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Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
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/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site 1: Smal; Library of
chromosomal fragments of L.Tactis strain MG1363 was
prepared by partial AluI digestion or by sonication.
                                                                                                                                                                                                                                                                                           181 CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                                                                                                                                                                                                                                                                                                                                                               241 TGGATCAACGICGICGIGGCAGTIGIGAIGACCGCATTGGCCATCAAACTGATGTTGATG
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
Contact: Sorokin A
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1. .664
/organism="Tetraodon nigroviridis"
/db.xref="taxon:99883"
/clone="032806"
/clone="15b="G"
/clone_lib="G"
/note="Genoscope sequence ID : COBGO
8 a 200 c 222 g 116 t 8 c
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                                                                                                                                                                                                      Score 44.4; DB 17;
Pred. No. 0.23;
0; Mismatches 129;
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Lactococcus lactis subsp. cremoris
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High quality sequence start: 30
High quality sequence stop: 3207.
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modified polylinker; Site 1: ECOR I; Site 2: Not I; UI-B-DW1 is a normalized cDNA library containing the following tissue(8): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contenins a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Dissovery in the Visual System, supported by National Eye Institute (NEI)."
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Tel: 319 335 8250
Emai: 319 335 9565
Email: msoarcs@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 617)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 CGCCAAGCCTGATCTGGTTCCCGCTGGTTTCGGCGCAGCAGCATTGTCACGCCCGC 217
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Program for Rat Gene Discovery and Mapping
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46.9%; Pred. No. 1.2;
tive 0; Mismatches 145;
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BM729055/c
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/dev stage="fetal" // Libb_host="DH10B" (Life Technologies) (T1 phage resistant)" // Libb_host="DH10B" (Life Technologies) (T1 phage resistant)" // Libb_host="DH10B" (Life Technologies) (T1 phage resistant)" // Libb_host="Dr20" (Libb_nost) (Libb_
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 TGGTCAACCGCAGCGTGCCCAGGTCGCTCTCGGGCGTGGTGGTGGTCTTGATGAAGTAGTGCG 358
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The following repetitive elements were found in this cDNA sequence: 148-171, >GC_rich#Low_complexity Seq primer: M13 Reverse.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
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46.9%; Pred. No. 1.9;
1.00 Mismatches 145;
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/clone="UI-B-EO1-aiw-a-06-0-UI"
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/tissue_type="fetal eye"
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                                                                                                                      Location/Qualifiers
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/clone lib="NIH MGC 9"
/tissue_type="adenocarcinoma cell line"
/lab host="nH10B (phage-resistant)"
/lab host="nH10B (phage-resistant)"
/noce="norgan: ovary; Vector: poTB7; Site 1: XhoI; Site_2:
FnocE="norgan: ovary; Vector: poTB7; Site 1: XhoI; Site_2:
Cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1: NBb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
47 a 245 c 277 g 101 t
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601593311F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947138 5',
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM819 row: p column: 23
High quality sequence stop: 765.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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46.9%; Pred. No. 2.2;
ive 0; Mismatches 145; Indels
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                                                                                                                                                                                                                               organism="Homo sapiens"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:3951622"
3mail: cgapbs-r@mail.nih.gov
fissue Procurement: DCTD/DTP
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/organism="Homo sapiens"
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/clone="IMAGE:3947138"
/clone="IMAGE:3947138"
/clone="Lib="NIH MGC 9"
/tissue_type="adenocarcinoma cell line"
/total host made by oligo-dT priming. Directionally
cloned into EcoRI/Xhol sites using the following 5,
adaptor: GGCACGAG(G). Size=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Supersorript II RT (Life Technologies)."
87 a 245 c 285 g 144 t
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Email: cgapbs-r@mail.nih.gov
Issue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 357)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM808 row: f column: 03
High quality sequence stop: 754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675 GCAGCGCCAGCGCCGAACTGCATCTCCACGTCCGCGAACCTGCGCGTCCTGCCGTTCA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 TGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCAT 277
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Pred. No. 2.3;
0; Mismatches 145; Indels
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Best Local Similarity 46.9%;
Matches 128; Conservative
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W91005 447 bp mRNA linear EST 12-SEP-1996 mf83h05.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:420921 5', mRNA sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 447)
Marria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified piT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 131 c 133 g 91 t
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The WashU-HMM Mouse BST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1406856.
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 9; Length 431;
Pred. No. 3;
                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGB:789032"
/clone=lib="soares_total_fetus_Nb2HP8_9w"
/dev stage="8-9 weeks"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 GCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCT 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                             /organism="Homo sapiens"
/db_xref="GDB:5986649"
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     High quality sequence stop: 426
                                     Location/Qualifiers
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1 Similarity 53.1%;
85; Conservative
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Fax: 314 286 1810
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W9f005/c
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with a modified polylinker; Plasmid DNA from the
normalized library NCT (GAP Pr22 was prepared, and se
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 431)
1 (Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Y., Washd-Merck EST Project 1997,
Unpublished (1997)
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbpp/image/image.html
www-bio.llnl.gov/bbpp/image/image.html
Insert Length: 423 Std Error. 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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zx41c05.81 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:789032 3', mRNA sequence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 40; DB 9; Length 357; ilarity 53.1%; Pred. No. 2.7; Conservative 0; Mismatches 75; Indels
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                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IWAGE:2110538"
/clone_lib="NCI_CGAP_Pr28"
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/lab_host="DH10B"
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AA452858.1 GI:2166527
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AI159901 504 bp mRNA linear EST 26-0CT-1998 qb55h08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704063 3' similar to TR:Q24551 Q24551 TENASCIN-LIKE PROTEIN. ;, mRNA
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 671 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 482.
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                    /organism="Homo sapiens"
/db xref="#GDB:5982951"
/db xref="taxon:9606"
/clone="IMAGE:785333"
/dev stage="8-9 weeks"
/lab_nost="DH108"
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             ity sequence stop: 443.
Location/Qualifiers
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1. (bases 1 to 463)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,Y., Waterston,R. and Wilson,R.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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4.6%; Score 40; DB 1
Best Local Similarity 53.1%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches
                                                                                                                                  db xref="taxon:10090"
                                                                                                                                                             clone="IMAGE:420921"
   location/Qualifiers
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135 c 141 g
                                                                                                 strain="C57BL/6J"
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Contact: Wilson RK
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Contact: Robert Strausberg, Ph.D.
Email: ggapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/lange/limage.html
Insert Length: 859 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 498.
                                                                                                                                                                                                              EST 21-DEC-1999
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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wj60d07.xl NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2407213 3'
Bimilar to TR:070465 070465 DOC4. ;; mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xef="taxon:9606"
/clone="IMAGE:2407213"
/clone=lib="NGI CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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Pred. No. 3.4;
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                                             /clone="IMAGE:2103625"
/clone=lb="MCI_CGAP_Brn23"
/Lissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                          GUNA LIDEALY Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.AG.B. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 684 Std Brror: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 485.

Location/Qualifiers
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 504)

NCI/NIDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Josocders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 ACCGCATTGGCCATCAAACTGATGTTGATGGGTTAGTTTTCGCGGGTTTTGGAATCGGTG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 CGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATG 270
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                                                                                                                                                                /clone="IMAGE:1704063"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 GCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCT 370
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53.1%; Pred. No. 3.3;
ative 0; Mismatches
                                                                                  organism="Homo sapiens"
db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 53.1%,
-hes 85; Conservative
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OY 331 GCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGAAATCT 370

Db 122 AGCACGGCCACCTTGATGCAGTCCTCGTTGGCGATGT 161

Search completed: April 27, 2003, 00:51:28 Job time : 1172.26 secs

· . .

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
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/label= LysE
complement (1723..2373)
ABK72786
AASS9552
AAT33536
AAI99683
AAI99682
                                                                         AAA52691
ABA90521
                                                                                                                                     AAH14671
AAH14183
ABL65724
AAQ22069
AAH66637
AAF72186
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AAR72186
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AA199682
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AAH14096
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ABL28046
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ABN18439
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complement (82..954)
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   /*tag= a
/label= LysG
1016..1726
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/label= orf3
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4.3 4403765 7
4.3 4411529
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Corynebacterium gl
Corynebacterium gl
Corynebacterium gl
C glutamicum gene
C glutamicum codin
C thermoaminogene
Escherichia coli g
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C glutamicum codin
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10233.535 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (19122) (ggdata/genseg/gensegen-embl/NA1981 DAT:*
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                                                                                                    April 26, 2003, 17:06:23 ; Search time 192.113 Seconds
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873
1 gtcgataagcagcgggtttg........ctgtgagctctggaccgtag
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.: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.
              GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 1008
Listing first 45 summaries
                                                                      nucleic search, using sw model
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AAF68077
AAF71779
AAS098_
AAH68420
AAH45375
AAG55755
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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95DE-1048222

22-DEC-1995; 26-JUN-1997.

568 404.2 326 326 303 193.6 71.6

Pred. No.

Result No.

Carbonic-anhydrase Carbonic-anhydrase Cglutamicum codin Corymebacterium gl Corymebacterium gl Cglutamicum codin Micromonospora DNA Mycobacterium tube Mycobacterium tube Mycobacterium tube Bndo-beta-N-acetyl Pseudomonas sp hea Drosophila melanog Drosophila melanog

Hydroxylase gene. Human cytoskeleton Pseudomonas aerugi Human ORFX ORF161 Human ORFX polynuc

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Lung cancer relate

Mycobacterium tube Mycobacterium tube Escherichia coli y

Propionibacterium BCG deletion regio

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium gluteamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L.lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
1961 TGCCCGCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTC 2020
                                                                                                                                                                                                                                                                                                                             AGATATTTGTCCGTGAGCAGGCCCTGCGCAAGTGGTGGTGAGAAAGCAATGACGCCAAGACAA
                                                                                                                                                                                                                                                                                                       TTAATGATGGAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCTCCGCCATGAAC
                                                                                 2021 AACATGCCCTCAGACAGGGACTTACCCTGGCTGGCGGGGAACCCTCTGGAATTCCATCG
                                                                                                                                                                                                                                                            2141 TTGTTGGCAGCTGACTGCAACAAGTTCTCACGGTCATCGCCGGTTCCTCCACCAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C glutamicum coding sequence fragment SEQ ID NO: 7063.
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                                                                                                                                                                                                                                                                                                                                                                                                                   2261 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 2293
                                                                                                                                                                                                                                                                                                                                                                                          841 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ando S, Hayası
da M. Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH68528 standard; DNA; 349980 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000JP-0280988.
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2000JP-0159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mizoguchi H
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa S,
Tateishi N,
                                                                                                                                                                           2081
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                                                                                                                                                                                                                                                                                                                                        This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Export of (A) has been found to depend on a single gene. NB. This sequence has been created from the information given in table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1540
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                                                                                                                                                                                        Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGCCGCGTCGGCGTCGCGCAATACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 873; DB 18; 100.0%; Pred. No. 7.3e-247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                          GMBH.
                                                                                                                                                                                                                                                                                                  Claim 23 and 26; Page -; 16pp; German
                                        (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                     Vrlijc M
95DE-1048222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity .... Matches 873; Conservative
                                                                                   Eggeling L, Sahm H,
                                                                                                                           WPI; 1997-333867/31.
P-PSDB; AAW37714-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                          Corynebacterium
22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.

Corynebacterium glutamicum.

EP1108790-A2

20-JUN-2001.

coding sequence fragment SEQ ID NO:

C glutamicum

(first entry)

26-SEP-2001

AAH68419;

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                                                                                                                                                                                                        Db 128548 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGATTG 128489
                                                                                                                                                                                                                                                                                               Db 128428 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTTCGCGGCAGCCTGATCTGGTTCCCG 128369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 128308 TGGATCAACGTCGTCGTGCCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 128249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128309
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                                                                                                                                                                                          9
                                                                                                                                               0; Gaps
specification, but was obtained in electronic format directly from Buropean Patent Office.
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                                                                                                                                                                                   1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG
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                                                                                                         Length 349980;
                                                             Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 other
                                                                                                                                               Indels
                                                                                                                                                 ö
                                                                                                     Query Match
100.0%; Score 873; DB 22;
Best Local Similarity 100.0%; Pred. No. 6.1e-246;
Matches 873; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127708 TCAGCCGCCTCCGCTGTGAGCTCTGGACCGTAG 127676
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

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Yokoi

Ochiai K,

S, Hayashi M, Ozaki A;

Mizoguchi H, Ando Senoh A, Ikeda M,

Nakagawa S, Tateishi N,

WPI; 2001-376931/40. P-PSDB; AAG93200.

16-DEC-1999; 99JP-0377484. 07-APR-2000; 2000JP-0159162. 03-AUG-2000; 2000JP-0280988.

18-DEC-2000; 2000EP-0127688

(KYOW) KYOWA HAKKO KOGYO KK

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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform particularly L. lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 GTTTTCGCGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 AATCTCATCGATCGCCTCCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 GITITCGCGGGITITGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 AATCTCATCGATCGCCTCCAACTCGGCGTCAGAAAACTCCAAGTTGTTGAGTGAATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGTACTCTCCTTGCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO: 3454; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 627 BP; 139 A; 159 C; 185 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.1%; Score 568; DB 22; L
100.0%; Pred. No. 3.4e-157;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 486 (
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RESULT 3 AAH68419/c ID AAH68419 standard; DNA; 627

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                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
                                                                                                                                845
                                665
                                               268
                                                                725
                                                                               208
                                                                                               785
               328
                                                                                                               207 GCCAGCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAAT 148
                                                                                                                                               88
                                                                                                                                        GATGGAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGC
         387 GCGTTCCTGGGCGATGTCATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACAT
                               GCCCTCAGACAGGGACTTACCCTGGCTGGCGGGAACCCCTCTGGAATTCCATCGAGATA
                                               GCCCTCAGACAGGGACTTACCCTGGCTGGCGGGGAACCCTCTGGAATTCCATCGAGATA
                                                                              267 TTTGTCCGTGAGCAGGCCCTGCGCAAGTGGTGAAAGCAATGACGCCAAGACCATTGTT
                                                                                               GGCAGCTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAAT
                                                                                                                               GATGGAATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGC
                                                                                                                                                                                                                                                                       Corynebacterium glutamicum MCT protein encoding DNA SEQ ID NO:669
                                                               TITIGICCGICAGCAGCCCTGCGCAAGIGGTGAGAAAGCAAIGACGCCAAGACCATIGII
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                                                                                                                                                                CGCCTCCGCTGTGAGCTCTGGACCGTAG
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99DB-1032230
99DB-1032230
99DB-1033005
99DB-1040764
99DB-1040765
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99DB-1031454.
99DB-1031547.
99DB-103122.
99DB-1032124.
99DB-1032128.
99DB-1032128.
99DB-1032128.
99DB-1032180.
99DB-1032180.
99DB-1032180.
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99DE-1032227.
99DE-1032228.
                                                                                                                                                                                                      RESULT 4
AAF68077/c
ID AAF68077 standard; DNA; 993
                                                                                                                                                                                                                                                                                                                                                                                      2000WO-IB00926
                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                     WO200100805-A2.
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27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000;
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or ridentification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGCGGCCCCTCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTGTGAGCTCTGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 AGCACCAATCAATGCACTGGTCACGGTA--TCCGCGCCGTACTCTCCTTGCTCGCGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 ACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTCATCGCCCCGGTTCCTCCACCCAACGATTAATGATGGAATAGCTTGGCTGATGAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Length 993;
                                                                                                                                                                                                                                                                                                                                   Haberhauer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 993 BP; 222 A; 247 C; 277 G; 247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 404.2; DB 22
Pred. No. 7.9e-109;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 1107-1108; 1119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.3%; Scc.larity 98.8%; Pre
Conservative 0;
                                            99DE-1040833.
99DE-1041378.
99DE-1041379.
99DE-1041395.
99DE-1042077.
99DE-1042078.
99DE-1040831.
99DE-1040832.
                                                                                                                                                                                                                            99DE-1042088
                                                                                                                                                                                                                                                                                                                                   Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-071486/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 418; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAB76844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transformation -
                                                                                                                                                                                                                                                                                    AG.
                                                                                                                                                                                                                                                                              (BADI ) BASF
                                               27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
03-SEP-1999;
27-AUG-1999;
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03-SEP-1999
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TAG 873

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Haberhauer

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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                             Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTTATCGGCGGCGTCGGCGCGCAATACGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATCAACGTCGTCGTGGCAGTTGTGATGACGCATTGGCCATCAAACTGATGTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACACCGGACGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617 GACACCGGACGGTGGATTTTTCGCCGCTGCCGCGCAGCGGCAAGCCTGATCTGGTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCCATCAAACTGATGTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 326; DB 22; Length 822; 100.0%; Pred. No. 8.2e-86; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;
                                                                                                                                                                                       Zelder O,
                                                                                                                                                                                                                                                                                                           Claim 3; Page 233-234; 1737pp; English.
                                                                                                                                                                                      Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTAGTTTTCGCGGGTTTTTGGAATC 326
                99DE-1041396.
99DE-1042076.
99DE-1042077.
99DE-1042086.
99DE-1042086.
                                                                                                  99DE-1042095.
99DE-1042124.
99DE-1042129.
                                                                                                                                         2000US-0187970
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2002 (first entry)
                                                                                                                                                                                     Pompejus M, Kroeger B,
                                                                                                                                                                                                           WPI; 2001-137957/14.
P-PSDB; AAB79660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS96098 standard;
                                                                                                                                                              (BADI ) BASF AG.
                31-AUG-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                  03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
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AAS96098
ID AAS9
XX
AC AAS9
XX
CDT 26-F
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                                                                                                                                                      Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; libid; saturated fatty acid; unaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                  Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53
                                                         AAF71779 standard; DNA; 822 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99DE-1031465.
99DE-1031478.
99DE-1031510.
99DE-1031541.
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99DE-1031632.
99DE-1031632.
99DE-1031636.
99DE-1032125.
99DE-1032126.
99DE-1032130.
99DE-1032130.
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99DE-1032228.
99DE-1032229.
99DE-1032230.
                                                                                                                                                                                                                                                                                                    23-JUN-2000; 2000WO-IB00923
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                                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                         30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                              04-JAN-2001
                                                                                  AAF71779;
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Gaps

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RESULT 7

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                                                            methionine biosynthesis pathway; large-scale production of fine chemical; Corynebacterium diphtheriae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lyshe and methionine biosynthetic pathways. The polynucleotide sequences of the invention of expression of for the large-scale production and/or anoulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. c. diphtheriae in a subject to detect diphtheria.

AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention.
                                                                                                                                                                                                                                                                                                                             Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 796
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                                                                                                                                                                                                                                                                                                                             Haberhauer G,
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0
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                                               Metabolic pathway protein; MP; lysine biosynthesis pathway

    C. glutamicum gene #23 encoding metabolic pathway protein.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;
                                                                                                                                                                                                                                                                                                                             Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 214-215; 316pp; English.
                                                                                                                                                                                                                                                                                                                             Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium and Brevibacterium -
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                                                                                                                                                                                                                                              09-MAR-2000; 2000US-187970P.
23-JUN-2000; 2000US-0606740.
                                                                                                                                                                                                               22-DEC-2000; 2000WO-IB02035
                                                                                                               Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                             Kroeger
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Matches 326; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU71888
                                                                                                                                                                                                                                                                                                                                             Hwang B;
                                                                                                                                                                                                                                                                                             (BADI ) BASF AG
                                                                                                                                               40200166573-A2
                                                                                                                                                                               13-SEP-2001
                                                                                                                                                                                                                                                                                                                             Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                             Lee H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, utamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGCTGGTTG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACCCGAATGCGTATTTGGACGCGTTTGTGTTTATCGGCGCGCGTCGGCGCGCATACGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGGCAAGCCTGATCTGGTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi
                                                                                                                                                                                  amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO: 3455; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                        C glutamicum coding sequence fragment SEQ ID NO: 3455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 708 BP; 134 A; 173 C; 221 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 303; DB 22;
Pred. No. 4.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%; Pred. No. 4.6
Matches 303; Conservative 0; Mismatches
                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
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03-AUG-2000; 2000JP-0280988.
                  AAH68420 standard; DNA; 708
                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                   organic acid synthesis; ds.
                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Patent Office.
                                                                                                                                                                                Coryneform bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
                                                                                                  26-SEP-2001
                                                                                                                                                                                                                                                                                                                          20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa S,
Tateishi N,
                                                          AAH68420;
AAH68420
                                                                                                                                                             셤
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The nucleotide sequence of a 5541 bp probe obtained by digestion of Escherichia coli genomic DNA with the restriction enzyme HindIII. The probes (AAQ55133-48 and AAQ55752-58) represent other probes derived, by HindIII digestion of the genomes of Staphylococcus aureus, S.epidermis, Enterococcus faccalis, Pseudomonas aeruginosa, E.coli, Klebsiella pneumoniae or Enterobacter cloacae. The probes can be used to detect their respective microorganisms in clinical samples.
2687 CATTATCCATCTGACGTTTGTGCTCTCTGCATTTGTGATGGGCTATCTTGACCGACTGAC 2746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2807 TATCGGAAGACGCCTGCCACAGATTCAGCTCGCCATCGGCGATATGCTGATCAATCTGCG 2866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2867 CCAGCTCCTCGGTGCTAAATGTCAGATTATTCAGCGCCTGCACGTTCTCCTCAAGTTGTC 2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 CATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1417 ATAGGTGTGGCCGTGGTGCTCACCGGATTGGCCGTGAGCTGATCCTGATGGCTTA 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTGATGACCGCATTGAACTGATGTTGATGGGTTAGTTTCGCGGGTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACTCGGCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCT
                                                                                                                                                                                                                                                                                                           P.aeruginosa; E.coli;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe for identifying bacteria causing infectious disease - consists of a DNA fragment obtained by HindIII cleavage of the pathogenic bacterial genomic DNA
                                      250 GICGICGICGCAGITGICAIGACCGCAITGGCCAICAAACIGAIGITGAIGGGITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5541 BP; 1331 A; 1353 C; 1417 G; 1440 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.6; DB 15;
Pred. No. 1.8e-10;
0; Mismatches 299;
                                                                                                                                                                                                                                                                                                       Probe, S.aureus, S.epidermis, E.faecalis,
K.pneumoniae, E.cloacae, clinical sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uehara H;
                                                                                                                                                                                                                                                                    Escherichia coli genomic probe EC-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 70-73; 100pp; Japanese.
                                                                                                                                                               BP.
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                                                                                                                                                               AAQ55755 standard; DNA; 5541
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Similarity 49.4%;
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                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eda S, Matsuhisa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-035086/04.
                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1992;
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                                                                                                                                                                                                  AAQ55755;
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                                                                                                                           RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin biosynthetic enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present sequence encodes an enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 CAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCCGCTGGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-resistant; lysin biosynthesis; enzyme; coryneform; aspartate-semialdehyde dehydrogenase; lysB; ds.

    C. thermoaminogenes lysin biosynthetic enzyme lysE DNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 193.6; Di
Pred. No. 1.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 22-24; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium thermoaminogenes.
                                                                                                                                                                                                                                                                               AAH45375 standard; DNA; 1568 BP.
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Best Local Similarity 78.4%;
Matches 232; Conservative
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P-PSDB; AAG64047.
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                                                                                                                                                                                        708
                                                                                                                                                     GGT 303
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The invention describes a method of monitoring differential expression of
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                                                                                                                                                        CATTCAATAAGTGTAGGCTGTTGAGGTTGGCTTCGGTAAGCATTTTCGGCGTCAGACCAC 3087
                                                                                                                                                                                                                     3088 GAACTITATICCCTTCACGATGCATCCGTGAATCTTGCGGAATGCCGTTGAGATATTTC 3147
                                                                                                                                                                                                                                                                                   CGGTCAGCAATCCCTGAGCCAGAGGAGATAAAGGCAATACAGCCCACGCGGTTATTTTGCA 3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                     CCGTGAGCAGGCCCTGCGCAGTGGTGAGAAACAATGACGCCAAGACCATTGTTGCCAG 730
                                                                                                                          CATTGAGCTTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACT
                                                                                                                                                                                                                                                                                                                  731 CTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGG
                                                                                                                                                                                                                                                                                                                                                                               791 ANTAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCCATGAACTCAGCCGCCT
443 CAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCCGTACTCCTTGCT
                                                             CGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGGCGATGT
                                                                                           Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis genomic sequence tag (GST)
                2927 CGCGCGC-TGCCACCAATCAATACCGACGTCACGCGATCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 77; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3313 TTTGCGTCCGCTCTGGCGAGTA 3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                851 CCGCTGTGAGCTCTGGACCGTA 872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK72786 standard; DNA; 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2001; 2001WO-US31437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced tag array
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coher Bacillus cells comprising labelled nucleic acid probes isolated from Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus commic sequenced tags (GST), examining the array, and determining captures sequenced tags (GST), examining the array, and determining captures array. The method is useful for measuring the expression of ganes in a first Bacillus cells relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes computed in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way in expression of genes or other physiological provocation. Extensive collow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; BLISh; inflammatory lesion; acne vulgaris; ensyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 575 IGGATGAGGAGCGGAATCCCGTATTCTTGCAAAATATCAGCCGCCTTTTCGGTCTGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCAGGCTATCGCCCATTTGCGGAAGAGACTGGCCGCGTTCGGCAGCCACTTGATTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 TTGCGGACCTTGCCGAGCACGTCTTCTGTGATGCCCTCGGCCTGCAAAAACGGACTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 TGGGCAAGAGGTGTAAACGCGGATCGCCCCGGCTCCTTTTTT------CTGCAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGGAATAGCTTGGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 ACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - CCTGGCTGGCGCGGGAACCCTCTGGAATTCCATCGAGATATTTGTCCGTGAGCAGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%; Score 65.4; DB 24; Length 988; Best Local Similarity 55.3%; Pred. No. 5.9e-09; Matches 204; Conservative 0; Mismatches 141; Indels 24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 988 BP; 274 A; 247 C; 254 G; 213 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР.
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7642 GCGGCTGGTGGATGAGTAACGGGGTGCCAAGGTCACGCGCAATGGTGGCAGCACGTTCTG 7583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presence or absense of deletion junctions (see AAT31538-46), or by detecting the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of
           797 TTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCTCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         verecting markers for avirulence in Mycobacterium - used in
production of vaccines against bacterial infection, and to detect
bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCG delta 2; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.5%; Score 57; DB 17; Length 15239; Best Local Similarity 53.1%; Pred. No. 5.6e-06; Matches 145; Conservative 0; Mismatches 125; Indels 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "BCG delta 1 deletion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCG deletion region 2 and flanking sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAS59506-AAS59804 represent DNA molecules encoding
Propionibacterium acnes immunogenic polypeptides. The proteins and their
Bropionibacterium acnes immunogenic polypeptides. The proteins and their
CC diagnosis of medical conditions caused by P. acnes. The disorders include diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and concern in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme in AAUSIG63-AAUSI893 and AAUG753.

Note: The sequence data for this patent did not form part of the printed can the wire, in for while the minimal in electronic format directly from MIPO at the printed as the wire in the sample of the printed as the wire the printed as the minimal process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGA
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Best Local Similarity 51.6%; Pred. No. 4.5e-06;
Matches 194; Conservative 1; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wany ...
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e J, Zhang Y, Jen S,
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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Propionibacterium acnes
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium by determining the muclectide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the mucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of the tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                     145
                                                                                                                                                                                       TGTCACGCCCGCTGTCCAAGCTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; d
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Score 57; DB 22; Length 4403765; Pred. No. 6.3e-05;

6.5%;

Query Match Best Local Similarity

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2227633 AGGICCIGGIGACCIGIGGGGCATICACGIICCICAACCCACACGICIACCICGACACCG 2227692
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                                                                                                                                                                                                                                                          206 TGTCACGCCCCCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTGGCAGTTG 265
                                                                                    TTGTGTTTTATCGGCGCGCGCGCGCATACGGCGACACCGGACGGTGGATTTTCGCCG 145
26 AGCCCATGTTGATGGCAATCGTGTCTGATTGAACCCGAATGCGTATTTGGACGCGT 85
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epidemiology; patient treatment; epidemic monitoring; d
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expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
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                                                                                                                                                                                                                                                                                                                                                   353 reaccreacreaarccecarerraccreaaracriristreracreescasccrresce 412
                                                                                                                                                                                                                                                                                                                                                                                                       110 CGCAATACGGCGACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 TGTGGTTCTTTGGTCTGTTCTCGCAGCCTGGCTGGCACCGCGTCTGCGCACGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCACAGCGCATTATCAATCTGGTTGTGGGATGTTTATGTGCGTTTTATTGCCAGC
                                                                                                                                                                                            Query Match 6.5%; Score 56.4; DB 21; Length 636; Best Local Similarity 52.1%; Pred. No. 2.2e-06; Matches 126; Conservative 0; Mismatches 116; Indels 0
                                                                                                                                           Sequence 636 BP; 120 A; 143 C; 180 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 27, 2003, 00:06:32 Job time : 5330.11 secs
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                                                                                                                                                                                                          Db 2230334 AGGICCIGGIGACCTGTGCGGCATTCACGTTCTCAACCCACACGTCTACCTCGACACG 2230393.
                                                                                                                                                                                                                                                                                                          Db 2230394 TCGTGTTGCTAGGCGCGCTGGCCAACGACACAGCGA---CCAGCGCTGGCTGTTCGGCC 2230450
                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 2230511 TGCGCGGCTGTTCACCAACCCCGGCTCGTGGAATCCTCGACGCCCTGATCGCGGTCA 2230570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the yggA gene (an excretion protein gene) of Bscherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      146 CTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTTTCGGCGCAGCAT 205
                                                                                                                                                                                                                                                                 206 TGTCACGCCCGCTGTCCAGCCCCCAAGGTGTGGCGCTCGATCAACGTCGTCGTGGCAGTTG 265
                                                                                                                                                         26 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. coli; yggA gene; amino acid production; excretion protein gene;
amino acid excretion protein; ds.
                                                            Length 4411529;
                                                    Query Match 6.5%; Score 57; DB 22; Length 44 Best Local Similarity 53.1%; Pred. No. 6.3e-05; Matches 145; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 2230571 TGATGGTTGCGCTGGGAATCTCGCTGACCGTGA 2230603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 TGATGACCGCATTGGCCATCAAACTGATGTTGA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..636
/*tag= a
/product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA52691 standard; DNA; 636 BP.
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99RU-0104431.
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P-PSDB; AAB01789.
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Tokhmakova IL;
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09-MAR-1999;
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sequence 21/1, Ap Sequence 21484, A Sequence 4745, Ap

Sequence 34, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3113, Ap Sequence 402, App Sequence 402, App Sequence 402, App Sequence 402, App

Sequence 10, App Sequence 10, App Sequence 28, Appl Sequence 10,

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Run on:

Sequence:

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Query Match 100.0%; Score 873; DB 9; Length 3309400; Best Local Similarity 100.0%; Pred. No. 7.6e-281; Matches 873; Conservative 0; Mismatches 0; Indels 0;
0 US-09-974-300-2171
0 US-09-864-761-21484
0 US-09-864-761-4745
0 US-09-745-763-198
0 US-09-864-761-19241
0 US-09-864-761-2513
US-09-712-363-57
                                                                                                                                                       US-09-664-761-20241
US-09-664-761-3471
US-09-9712-363-100
US-09-925-300-760
US-09-988-348-34
US-09-988-348-34
US-09-861-289-34
US-09-861-289-5
US-09-918-384-5
US-09-918-95-3113
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US-09-976-740-10
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-12-18
PRIOR PELION DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR SEQIENTING DATE: 2000-08-03
NUMBER OF SEQIENTING DATE: 2000-08-03
NUMBER OF SEQIENTING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIALI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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Sequence 1034, Ap
Sequence 1032, Ap
Sequence 592, App
Sequence 592, App
Sequence 439, App
Sequence 1, Appl
Sequence 1, Appli
Sequence 398, App
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Sequence 51, Appl
Sequence 7455, Ap
Sequence 77, Appl
Sequence 11, Appl
Sequence 15, Appl
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9634.930 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/PCT NEW PUB. seq:*
| cgn2_6/ptodata/2/pubpna/PCT NEW PUB. seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB. Beq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB. Beq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW PUB. Beq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW PUB. Beq:*
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                   GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-954-456-1034
US-09-738-626-1672
US-10-184-644-592
US-10-184-634-592
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US-09-774-300-77
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Listing first 45 summaries
                                                                                                         - nucleic search, using sw model
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Db 1328548 GTCGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACTGGTTG 1328489

1 GICGATAAGCAGCGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTG 60

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Sequence 188, App Sequence 398, App Sequence 8, Appli

US-09-738-626-1 US-09-815-242-7775 US-10-184-644-398

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Best Local Similarity 100.0%; Pred. No. 3e-180;
Matches 568; Conservative 0; Mismatches 0
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 3454
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US-09-746-660A-51
Sequence 51, Application US/09746660A
Sequence 51, Application WS/09746660A
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Roager, Burkhard
APPLICANT: Schroder, Harrwig
APPLICANT: Zelder, Oskar
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3454
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1328488 AACCCGAATGCGTATTTGGACGCTTTGTTTTTTTCGCCGCGTCGGCGCGCAATACGGC 1328429
                                                                                                                                     Db 1328428 GACACCGGACGGTGGATTTTCGCCGCTGGCGCTTTCGCGGCAAGCCTGATCTGGTTCCCG 1328369
                                                                                                                                                                                                                                                                  Db 1328368 Cresrederrrcescecaecackarrercaecececrerercaececeaeceaecece 1328309
                                                                                                                                                                                                                                                                                                                                                                                           Db 1328248 GGTTAGTTTTGGGGGGTTTTGGAATCGGTGGCCTTCGCCCAAATGTTGATGCCGGCGTCG 1328189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1328068 TCCGCGCCGTACTCTCCTTGCTCGCGCACCCCATGCAAGCGCCCATCTGCGCAAGTGAC 1328009
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                                                                                          121 GACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAGGCTGATCTGGTTCCCG 180
                                                                                                                                                                                                                181 CTGGTGGGTTTCGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTGTGCCCC 240
                                                                                                                                                                                                                                                                                                                                241 TGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGATGTTGATG 300
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APPLICANT: NAKAGNAA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: TOCHIAI, KEIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TARISHI NAOKO
APPLICANT: TREDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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Publication No. US20020197605A1
GENERAL INFORMATION:
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Fatent No. US20020146721A1
GENERAL INFORMATION:
FAPELICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: METHOD STORES: 200-US
CURRENT APPLICATION NUMBER: 09/680,598
FRIOR APPLICATION NUMBER: 09/680,598
FRIOR FILING DATE: 2000-10-06
FRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOUTHARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.6e-91
Matches 303; Conservative 0; Mismatches 0
                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES;
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626;
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
SOFTWARE: Patentin ver: 3.0
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                           AKIHIRO
MASATO
                                                                                                    AKIO
                                                                                             OZAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Coryr
US-09-738-626-3455
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## APPLICANT: Hwang, Byung-Joon
### TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
### FILE NET INVENTION: METABOLIC PATHWAY PROTEINS
### FILE NET INVENTION: METABOLIC PATHWAY PROTEINS
### CURRENT FILING DATE: 2000-12-22
### FILING APPLICATION NUMBER: 09/60740
### PRIOR FILING DATE: 2000-06-23
### PRIOR FILING DATE: 2000-06-23
### PRIOR FILING DATE: 1999-06-25
### PRIOR FILING DATE: 1999-07-02
### PRIOR FILING DATE: 1999-07-03
### PRIOR FILING DATE: 1999-07-08
### PRIOR FILING DATE: 1999-07-07-08
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37.3%; Score 326; DB 9; Length 822;
Best Local Similarity 100.0%; Pred. No. 5.4e-99;
Matches 326; Conservative 0; Mismatches 0; Indels
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US-09-738-626-3455
Sequence 3455, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MKLIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
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; OTHER INFORMATION: RXA01394
US-09-746-660A-51
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874 AGCGATCTGATAACAAGCCTTCTGATAACGGTCCGTATGCAATCAACCCGGCACCAT 818
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APPLICANT: Havukkala, 11kka
APPLICANT: Bloksberg, Leonard
APPLICANT: Lubbers, Mark
APPLICANT: Dekker, James
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Holland, Ross
O'Toole, Paul
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Best Local Similarity 49.3
Matches 176; Conservative
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APPLICANT:
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                                                                                                                                                                                                              857 AGCAGGCTATCGCCATTTGCGGAAGAGACTGGCCGCTTCGGCAGCCACTTGATTCAGC 798
                                                                                                                                                                                                                                                                                  TTGCGGACCATATCAATATTGTTCACGTTCAACATGCCCTCAGACAGGGACTTAC---- 625
                                                                                                                                                                                                                                                                                                                                                       797 TTGCGGACCTTGCCGAGCACGTCTTCTGTGATGCCCTCGGCCTGCAAAACGGACTGTTC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             737 GCATCAGCGGCTCTTGACCCGGGGAATCCCTGTCAAATATTTCGTTGTTAAAAGCCCCT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAGCTGACTGCAACAAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                            511 ACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGTCATTGAGC
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                                                                        Indels 24;
   Length 988;
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APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of
FILE REPERENCE: STAN102CON
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6.5%; Score 57; DB 9; Length 597
Best Local Similarity 53.1%; Pred. No. 8.4e-09;
Matches 145; Conservative 0; Mismatches 125; Indels
Score 65.4; DB 10;
Pred. No. 1.6e-11;
0; Mismatches 141;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 597
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CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
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US-09-894-844-11
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Patent No. US20020176873A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 55.3%;
Matches 204; Conservative
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APPLICANT: Coolbear, Timothy
IITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods
IITLE OF INVENTION: Using Them
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                                                                                                                       TGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCCGCTGGATCAACGTCGTCGTCGTGGCAGTTG 265
                                                                                                                                                                                               TGCGCGGGCTGTTCACCAACCCCGGCTCGTGGAGAATCCTCGACGGCCTGATCGCGGTCA 562
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365 AAATCTCATCGATCGCCTCCAACTCGGCGTCAGAAAACTCCAAGTTGTTGAGTGAATCAA
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CURRENT APPLICATION NUMBER: US/09/971,536
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
PRIOR APPLICATION NUMBER: PCT/NZ01/00160
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2001-08-08
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49.3%; Pred. No. 2.3e-06;
iive 0; Mismatches 163;
                                                                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1277
                                                                                                                                                                                                                                                                               TGATGACCGCATTGGCCATCAAACTGATGTTGA
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271 ACCGCATTGGCCATCAAACTGATGTTGATGGGTTAGTTTTCGCGGGTTTTTGGAATCGGTG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.6%; Score 40; DB 10; Length 431;
1 Similarity 53.1%; Pred. No. 0.0036;
85; Conservative 0; Mismatches 75; Indels
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 1672
: LENGTH: 948
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APPLICANT: SENOH, AKIHIRO
APPLICANT: KEDA, MASATO
APPLICANT: OZAKI, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1034
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; Sequence 1672, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-954-456-1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 85; Conserva
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Best Local Similarity
Matches 58; Conserv
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Patent No. US20020115057A1
GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE SPERENCE: 689280-76
CURRENT FILING DATE: 2001-09-18
CURRENT FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-28
PRIOR PAPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-28
PRIOR PALLING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/234,923
PRIOR PALLING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,134
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 GCCCGCTGTCCAGCCCCAAGGTGTGGCCGCTGGATCAACGTCGTGGTGGTGGTG 270
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                                                                                                                                                                                                                                                                                       APPLICANT: Feinberg, Andrew
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Jiang, Shan
TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
TITLE OF INVENTION: METHODS FOR ISLANDS
FILE REFERENCE: 0107.00128
CURRENT APPLICATION NUMBER: 105/09/661,893
CURRENT FILING DATE: 2001-05-22
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR PILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 40; DB 10; Length 399; 53.1%; Pred. No. 0.0035; vative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AGCACGGCCACCTTGATGCAGTCCTCGTTGGCGATGT 240
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                                                                                                                                                             Sequence 29, Application US/09861893
Patent No. US20020045257A1
GENERAL INFORMATION:
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Matches 85; Conservative
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; ORGANISM: Homo sapiens
US-09-861-893-29
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PILE REFERENCE: P3430R10217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ATACGGCGACACCGGACGGTGGATTTTCGCCGCTGGCGCGTTCGCGGCAAGCCTGATCTG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 RDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEPVEANSEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 GTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCATCAAACTGAT 293
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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PRIOR PLLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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Publication No. US20020197605A1
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Best Local Similarity 9.2%;
Matches 28; Conservative
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SENOH, AKIHIRO
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CURRENT APPLICATION NUME
CURRENT FILING DATE: 20
Zhang, Zemin
                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo Sapien
US-10-184-634-592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 GTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGCCCATCAAACTGAT 293
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4.2%; Score 36.4; DB 9; Length 4
Best Local Similarity 9.2%; Pred. No. 0.063;
Matches 28; Conservative 94; Mismatches 183; Indels
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o. US20030068684A1
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Wood, William I.
                                                                                                                                                                                                                                       Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L
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Wood, William I.
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                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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; ORGANISM: Homo Sapien
US-10-184-644-592
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                                                 Sequence 592, Applica
Publication No. US200
GENERAL INFORMATION:
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Publication No.
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Wall, Daniel Trawick, John D. Carr, Grant J. Yamamoto, Robert T. Xu, H. Howard

US20020061569A1

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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                              146 CTGGCGCGTTCGCGCCAAGCCTGATCTGGTTCCCGCTGGGTTTTCGGCGCAGCAT 205
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                                                            DB 9; Length 1068;
                                                    Query Match 4.1%; Score 36; DB 9; Length 106
Best Local Similarity 53.6%; Pred. No. 0.12;
Matches 75; Conservative 0; Mismatches 65; Indels
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Best Local Similarity 53.6%; Pred. No. 5.1;
Matches 75; Conservative 0; Mismatches
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 1
LENGTH: 3309400
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-439
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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Publication No. US20020197605A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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TT: OCHIAI, KEIKO
TT: YOKOI, HARUHIKO
TT: TATEISHI, NAOKO
TT: SENOH, AKIHRO
TT: IKEDA, MASATO
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                                                          Length 996;
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                                                        Score 35.4; DB Pred. No. 0.19; 0; Mismatches
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Job time : 3284.59 secs
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                                                    Query Match
Best Local Similarity 53.2%;
Matches 75; Conservative C
; LOCATION: (1)...(996)
US-09-815-242-7775
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RESULT 15 US-09-815-242-7775/c ; Sequence 7775, Application US/09815242

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ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
US-08-920-812-20
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MOLECULE TYPE: GE
ORIGINAL SOURCE:
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Sequence 20,
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Sequence 2,
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Sequence 3,
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                                                                                  April 26, 2003, 20:22:28; Search time 49.1862 Seconds
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    GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-920-828-20
US-08-930-878-17
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| Patent No. 5/53188
| GENERAL INFORMATION: APPLICANT: Ohno, Tsuneya APPLICANT: Ohno, Tsuneya APPLICANT: Uchara, Hirotsugu APPLICANT: Uchara, Hirotsugu APPLICANT: Eda, Soji TITLE OF INVENTION: Probe for Diagnosing Infectious Disease NUMBER OF SEQUENCES: 25
| CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago Sears Tower, 233 South Wacker Drive CITY: Chicago Sars Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America 21P: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812 FILING DATE: 29-AUG-1997 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/362,577 FILING DATE: 27-AMR-1995 ATTORNEY/AGENT INFORMATION: NAME: RID-LAURES, Li-HSien REGISTRATION NUMBER: 19036/32420 TELECOMMUNICATION NUMBER: 19036/32420 TELECOMMUNICATION NUMBER: 19036/32420 TELECOMMUNICATION NUMBER: 19036/32420
                                                      US-09-292-225-20

US-09-292-225-17

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US-09-292-225-16

US-09-471-033-39

US-08-471-033-42

US-08-471-044-42

US-08-463-483A-39

US-08-461-046A-39

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TELEFAX: 312/474-0448
TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
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         Length 5541;
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APPLICANT: Ohno, Tsuneya
APPLICANT: Watsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
CORRESPONDENCE ADDRESS:
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                                                                                              Indels
8.2%; Score 71.6; DB 1;
9.4%; Pred. No. 1.7e-11;
ve 0; Mismatches 299;
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STATE: 11linois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 5770375
GENERAL INFORMATION:
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Query Match 8.2%;
Best Local Similarity 49.4%;
Matches 337; Conservative
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US-08-920-827-20
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Pred. No. 1.7e-11;
0; Mismatches 299;
                                                                                                                                       FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MRR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                 UMBER: US/08/920,827
29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-625
                                                                                                                                                                                                                                                                                                     NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 49.4%;
Matches 337; Conservative (
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR EGG ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       : 312/474-6300
312/474-0448
                                                                                                                    APPLICATION NUMBER:
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US-08-920-827-20
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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; Patent No. 5807673
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APPLICANT: Watsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
IITLE OF INVENTION: Probe for
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NAME: Rin-Laures, Li-Hsien
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STREET: 65.
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                                                                            3253 TGTACGAAGGTTGATGAATTAACAGCGGAATTTTCCACTCGCGCAGCAACTCAACCATTT 3312
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                      791 AATAGCTTGGCTGATGAATCAGAAGCGGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCT 850
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8.2%; Score 71.6; DB 1; Length 5541;
Best Local Similarity 49.4%; Pred. No. 1.7e-11;
Matches 337; Conservative 0; Mismatches 299; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OP INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
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COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacherichia coli
; STRAIN: Clinical Isolate EC-625
US-08-921-177-20
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08921177
Patent No. 5798211
                                                                                                                                                                                                                                               3313 TTTGCGTCCGCTCTGGCGAGTA 3334
                                                                                                                                                                       851 CCGCTGTGAGCTCTGGACCGTA 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 190
IELECOMMINICATION INFORMATION:
TELEPHONE: 312/474-6301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
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ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ohno, 7
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TOPOLOGY: line
MOLECULE TYPE: G
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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2867 ccaecricercesaranercaentarreacecerecaerterecerearentes
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CCAACTCGCCGTCAGAAACTCCAAGTTGTTGAGTGAATCAAGGCTGTTGTCCAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                               563 CATIGAGCTIGCGGACCATATCATATIGITCACGTTCAACATGCCCTCAGACAGGGACT
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                                                                                                                                         CAACTGACGAAGCACCAATCAATGCACTGGTCACGGTATCCGCGCCGTACTCCTTGCT
                                                                                                                                                                                                                                                                                  503 CGCGCAGCACCCATGCAAGCGCCATCTGCGCAAGTGACTGCCCGCGTTCCTGGGCGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                            2927 cececec-recearcaarcaaraceacercacecarca---
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATM:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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Matsuhisa, Akio

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2867 CCAGCTCCTCGGTGCTAAATGTCAGATTATTCAGCGCCTGCACGTTCTCCTCAAGTTGTC 2926
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                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                      Length 5541;
                                                                                                                                                                                                                                                                                                                                                                                 Score 71.6; DB 1; Length 5 Pred. No. 1.7e-11; 0; Mismatches 299; Indels
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                                                                                                                                                                                                                                                    , OKCANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-625
US-08-362-577C-20
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Best Local Similarity 49.4%;
Matches 337; Conservative
                                                                                                                                                                                     linear
E: Genomic DNA
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                                                                                                           5541 base pairs
                                                                                                                                  TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DI
ORIGINAL SOURCE:
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 20, Application US/08920828 Patent No. 5853998 GENERAL INFORMATION: APPLICANT: Ohno, Tsuneya

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2687 carrarccarcreacerrrerecrererecarrrerearidecrarerreaceacreae 2746
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APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
IITLE OF INVENTION: Probe for Diagnosing Infectious Disease
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(COMPUTER READABLE FORM:

(COMPUTER: Floppy disk

(COMPUTER: Floppy disk

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(COMPUTER: Ploppy disk

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(COMPUTER: Floppy disk

(COMPUTER: PatentIn Release #1.0, Version #1.25

(CURSTENT APPLICATION DATA:

APPLICATION NUMBER: US/08/920,828

FILING DATE: 29-AUG-1997

CLASSIFICATION: 435
                                                                                                     SSEE: Marshall, O'Toole, Gerstein, Murray &
F: 6300 Sears Tower, 233 South Wacker Drive
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2927 cececése-redenécharcharaceacerchéecearch--
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Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Escherichia coli
Clinical Isolate EC-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rin-Laures, Li-Hsien
RATION NUMBER: 33,547
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Best Local Similarity 49.4%;
Matches 337; Conservative
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MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 hard
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STRANDEDNESS: double
                                                                           NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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US-08-920-828-20
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Sequence 1, Application US/09103840A Patent No. 6294328
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Matches 145; Conservative
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                                                                                                                                                                              206
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3028 CATTCAATAAGTGTAGGCTGTTGAGGTTGGCTTCGGTAAGCATTTTCGGCGTCAGACCAC 3087
                                                                                              3088 GAACTTTATTCCCTTCACGATGCATCCGTGAATCTTGCGGAATGCCGTTGAGATATTTTC 3147
                                                                                                                                                                                                                                       3253 TGTACGAAGGTTGATGAATTAACAGCGGAATTTTCCACTCGCGCAGCAACTCAACCATTT 3312
                                                                                                                                                                        3148 cecircaccaarcerreaccacacacacaacraaaccaaracaccecaccecerrarrreca 3207
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                                                                                                                                     CCGTGAGCAGGCCCTGCGCAAGTGGTGAGAAAGCAATGACGCCAAGACCATTGTTGGCAG 730
                                                                                                                                                                                                               731 CTGACTGCAACAAGTTCTCACCGTCATCGCCCGGTTCCTCCACCCAACGATTAATGATGG 790
                                                                                                                                                                                                                                                                                            791 AATAGCTTGGCTGATGAATCAGAAGCGGCAGCCCTCCTCCGCCATGAACTCAGCCGCCT 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08390878
Patent No. 5700683
GENERAL INFORMATION:
APPLICANT: SCHOOL, CHARLES K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 15239;
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 1; Le
Pred. No. 6.4e-07;
0; Mismatches 125;
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REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEPAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             3313 TTTGCGTCCGCTCTGGCGAGTA 3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-390-878-17
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Best Local Similarity 53.1%;
Matches 145; Conservative (
                                                                                                                                                                                                                                                                                                                                                                        851 CCGCTGTGAGCTCTGGACCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                         TACCCTGGCTGGC-
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-390-878-17/c
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Db 2227633 AGGTCCTGGTGACCTGTGCGGCATTCACGTTCCTCAACCCACACGTCTACCTCGACACCG 2227692
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                                                                                                                                                                                                                                                                                                       4615 TGCGCGGGCTGTTCACCAACCCCGGCTCGTGGAGAATCCTCGACGGCCTGATCGCGGTCA 4556
                                                                                                                                                                                                                               TGTCACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTG 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAS EQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 85
4732 TCGTGTTGCTAGGCGCCGCTGGCCAACGAGCACAGCGA---CCAGCGCTGGCTGTTCGGCC
                                                                           146 CTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGCTGGTGGTGTTCGGCGCAGCAGCAT
                                                                                                                                               1675 redecedededadecadrecedraredrireceaeceredesricedadecederia
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OTHER INFORMATION: "n" bases at various positions throughout the OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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Gaps

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Length 1935;

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1356 GATGCCACCGCAGCAGCTATGGCCAATGACCACGAGGACCTCCACCTTGAGGGCGCACAC 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 CAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGCAGTTGTGATGACCGCATTGGC 281
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                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
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US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.5%;
Matches 112; Conservative
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Best Local Similarity 49.1%;
Matches 105; Conservative
                                                             TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1935 base pairs
                                                                                                                                                                                                                                            nucleic acid
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                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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LOCATION:
US-08-492-027A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 2230334 AGGICCIGGIGACCIGIGGGGAITCACGITCCICAACCIACGICIACGICIGACACCG 2230393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 TTGTGTTTATCGGCGCGCGCGCGCGCAATACGGCGACCGGACGGTGGATTTTCGCCG 145
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                                                                                                             APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Dohn C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24364-20007.00
CURRENT PELLICATION WUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCGT 85
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/492,027A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 4; Les
Pred. No. 9.1e-06;
0; Mismatches 125;
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ADDRESSEE: Birch, Stewart, Kolasch and Birch, STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 2230571 TGATGGTTGCGCTGGGAATCTCGCTGACCGTGA 2230603
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Patent No. 5912333
GENERAL INFORMATION:
APPLICANT: Suzuki, Shoichi
APPLICANT: Burnell, James N
TITLE OF INVENTION: DNA Encoding Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
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NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.5%;
Best Local Similarity 53.1%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
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COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGGATGCGTATTTGGACGCG 84
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 TTTGTGTTTTATCGGCGCGTCGGCGCGCAATACGGCGACACCGGACGGTGGATTTTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4403765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.6; D
Pred. No. 5.4;
                                                                                                                   FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
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TOPOLOGY:
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                                         Db 720323 dcGrccacdarcdadaccrdcrdagcadaarrccacrdcrdcccarricrrccccac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 718890 GCGTCGACGATCGAGGACCTGCTGGGGGGGATTCCGCTGGCCGGTTTCTTCGCCGCCGGG 718831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GCTGGCGCGTTCGCGGCAAGCCTGATCTGGTTCCCGGTGGTGGGTTTCGGCGCAGCAGCA 204
  145 GCTGGCGCGTTCGCCGCAAGCCTGATCTGGTTCCCGCTGGTGGGTTTCGGCGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TITGIGITITALCGGCGGCGTCGGCGCGAATACGCCGACACCGGACGGTGGATTTTCGCC 144
                                                                                                                                                                                                                                                                                                                                        APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: PURTER, Claire M.
APPLICANT: URVERT, Claire M.
TITLE OF INVENTION: JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNDEER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                  Db 720263 GAGATCGGCCGGTCGCGGGCCAACGCGTTGCACGGTTTACCGCGTCGATGGC 720208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAACCCGAATGCGTATTTGGACGCG 84
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                                                                                         205 TIGICACGCCCGCTGTCCAGCCCCAAGGTGTGGCGCTGGATCAACGTCGTCGTGGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 TIGICACGCCCGCTGICCAGCCCCAAGGIGIGGCGCTGGATCAACGICGTCGTGGC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.6; DB 4; Length 4411529;
Pred. No. 5.4;
0; Mismatches 124; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Nixon & Vanderhye
1100 No. 6004550th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                 APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
TITLE OF INVENTION: Intracellula
TITLE OF INVENTION: G2 in enzyme
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Patent No. 6004550
GENERAL INPORMATION:
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STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 47.5%;
Matches 112; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
STREET: 1100 No. 600
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN,
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APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1950 TCGATGCATCGCTGCCGGCCTCGGCTCAGGCAGAAGGCGCCGAGCATCCGGCCCT 1891
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0; Mismatches 106; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/775.245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/776,251
FILING DATE: 31-GAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Nixon & Vanderhye STREET: 1100 No. 6025340th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.4;
Pred. No. 1.
                                                                               FILING DATE: 30-JAN-1997
CLASCHFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01783
FILING DATE: 27-JUL-1995
PRIOR APPLICATION DATE: APPLICATION NUMBER: GB 9415167.7
FILING DATE: 27-JUL-1994
ATTORNEY AGENT INFORMATION:
                                              30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT/GB95/01782
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OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-776-251-1/c
; Sequence 1, Application US/08776251
                                                                                                                                                                                                                                                                                       NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.9%;
Best Local Similarity 48.0%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          2048 base pairs
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APPLICATION NUMBER: E
FILING DATE: 27-JUL-1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Va
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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1613 TGGGAGGCGATCGAGCACGCGGGCATCGACCGGCCGAGGCCTGAAGGGCAGCGGCCT 1668
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MOLECULE TYPE:
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sTRANDEDNESS:
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ORGANISM: PS
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FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
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LOCATION:
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                                                                              US-07-945-283-1
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                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1890 GCGCCAGCGGCTCGAGCCACTGCTTCTTGCTGCCGTTGCCGTAGCGCATGAGGATGG 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 TICCCGCTGGTGGGTTICGGCGCAGCATTGTCACGCCCGCTGTCCAGCCCCAAGGTG 234
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APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REPERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: 05/90/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver: 2.1
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                                                                                                                                                                                                                                                                                                               DB 3; Length 2048;
                                                                                                                                                                                                                                                                                                               Score 34.4; DB 3; Length 2 Pred. No. 1.4; 0; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                        NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REPRENNCE/DOCKET NUMBER: 620-20
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2048 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                      GB 9415167.7
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; ORGANISM: Streptomyces narbonensis
US-09-434-288-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 AACCCTCTGGAATTCCATCGAGAT 664
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Patent No. 6303767
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                                                                                                                                                                                                                                                                                                               Query Match 3.9%;
Best Local Similarity 48.0%;
Matches 98; Conservative
                                      FILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4*
    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1681
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6434 GCCCGACCGGGGGACCCGGCCGGGACCCGGGCTCGTCCTCCTCCTCGTCTTCGTCG 6493
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                                  GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EPO and LLT Genes
NUMBER OF SEQUENCES: 7.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                         E: Curtis P. Ribando
1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        OUTING DATE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
RGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
Sequence 1, Application US/07945283
Patent No. 5352596
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replace(7010, "g")
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replace(1381,
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SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pair
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                                                                                                                                                                                                                                                                          ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 78; Conserv
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OY 397 GARAACTCCAAGTIGITGAGAGATCAAGGCIGITGTCCAGCTGCTCAACTGACGAAGCA 456

Db 6494 ICTAGCACCACGATCTCGCCCGAGGCGGCGGCGCTGCTGCTGCGCCGAAGGA 6553
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⁴⁵⁷ CCAATCAATGCACTGGTCAGGGTATCGGGGC 488 q

Search completed: April 27, 2003, 07:20:35 Job time : 12814.2 secs

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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.

OM protein - protein search, using sw model

April 24, 2003, 18:21:23 ; Search time 19 Seconds (without alignments) 1194.091 Million cell updates/sec Run on:

US-09-105-117K-2 1191 1 WVIMEIFITGLLLGASLLLS......INVVVAVVMTALAIKLMIMG 236 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMM	SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	. GI		Description
-	350	29.4	211	Ħ	OOECSA		hypothetical 23K r
7	347	29.1		~	AH0874		probable membrane
e	343	28.8		~	B91103		hypothetical profe
4	340	28.5		~	E85948		
Ŋ	335	28.1	205	7	AG0112		
9	332	27.9		~	D83100		probable transport
7	326.5	27.4		7	C97472	•	
80	326.5	27.4		~	AG2690		LysE family transf
6	319	26.8	201	7	C70744		hypothetical profe
10	318	26.7	199	7	H70756		
11	302.5	25.4	204	~	AD3411		
12	245.5	20.6	211	~	B82318		E
13	238	20.0		7	S57940		Yada profein homol
14	176.5	14.8		~	D69838		conserved hypothet
15	173.5	14.6	210	~	F64609		conserved hypothet
16	170.5	14.3	210	N	B71906		hypothetical prote
17	164	13.8	205	~	B89854		conserved hypothet
18	154.5	13.0	205	N	C97219		uncharacterized or
19	153.5	12.9	213	N	E97789		hypothetical prote
20	151.5	12.7	208	Н	B69066	ļ	conserved hypothet
21	148	12.4	200	N	G83703		hypothetical prote
22	136.5	11.5	213	N	F83444		
23	132	11.1	210	~	E87252		
24	130	10.9	210	~	D84016		hypothetical prote
25	120.5	10.1	208	~	G87305		efflux protein, Ly
26	119	10.0	620	~	F82449		potassium uptake r
27	117.5	9.9	197	~	B83280		hypothetical prote
28	115.5	9.7	216	~	AH3203		RhtB family transc
29	114.5	9.6	208	7	G84086		dihydrodipicolinat

186 AFAASLIWPPLVGFGAAALSRPLSSPKVWRWINVVVAVVWTALAIKI 232 :|| :|| :|| :|| :|| 152 IISASFLWFFGLALLAAWLAPRLRTAKAQRIINLVVGCVWWFIALQI 198

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efflux protein, Lv	hypothetical prote	RhtB family transp	probable membrane	probable amino aci	probable hyuE APE1	RhtB family transp	conserved hypothet	branched-chain ami	hypothetical prote	threonine efflux p	iron(III) dicitrat	hypothetical prote	conserved hypothet	threonine efflux p	yfuD protein [impo
E87264	F97679	AD2904	AD0714	A96009	E72615	AB2683	H97464	H69277	G83082	A98223	G98273	AG3010	B83356	AH0466	T43921
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222	235	235	212	218	450	203	239	284	210	206	349	349	205	206	212
9.5 222 ;	9.5 235	9.5 235	9.3 212	9.2 218	9.2 450	9.1 203	9.1 239	9.0 284	9.0 210	8.8 206	8.8 349	8.8 349	8.7 205	8.6 206	8.6 212
113 9.5 222 ;	113 9.5 235	113 9.5 235	111 9.3 212	9.5	109.5 9.2 450	9.1	9.1	9.0	9.0	8.8	104.5 8.8 349	8.8	8.7	102 8.6 206	9.8

ALIGNMENTS

OURCEAR DESCRIPTION (SDM-fba intergenic region) - Escherichia coli (strain K-12) CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: Bacherichia coli CiSpecies: 11-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002 CiAccession: B65077; S04736
C; Species: Bscherichia coli C; Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002 C; Accession: B65077; S04736 R; Blattner, F.R.; Flunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Residues: 1-211 cBLAT-A; A; Rossidues: 1-211 cBLAT-A; A; Rossidues: 1-211 cBLAT-A; A; Residues: 1-211 cBLAT-A; A; Residues: 1-211 cBLAT-A; A; Residues: 1-212, Substrain MG1655 A; Experimental source: strain K-12, substrain MG1655 A; R; Afefounder, P. S; Perham, R. N.
C; Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002 C; Accession: B65077; SQ136 C; Accession: B65077; SQ136 A; RJBLattner, F. R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: DNA A; Residues: 1-211 cBLAT- A; Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A; Experimental source: strain K-12, substrain MG1655 A; Referenceder, P. R.; Perham, R. N. Maicrobion C; A; Perham, R. N.
Riblatiner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. S.; Rose, D.J.; Mau, B.; Shao, Y. Science 27., 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65077 A;Accession: B65077 A;Accession: B65077 A;Kesidues: 1-211 <blaty 1-211="" <blaty="" a;="" a;cross-references:="" a;experimental="" a;kesidues:="" a;reformeder,="" gb:ae000375;="" gb:u00096;="" k-12,="" mg1655="" mg1655<="" nid:g1789282;="" p.s.;="" perham,="" pid:g1789290,="" pidn:aac75960.1;="" r-12,="" r.12,="" reperimental="" source:="" strain="" substrain="" td=""></blaty>
Science 77, 1453-1462, 1997 Science 77, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65077 A;Accession: B65077 A;Residues: 1-211 cBLATA A;Residues: 1-211 cBLATA A;Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A;Referenced: Britain K-12, Substrain MG1655 A;Referenced: CBCATPAM, R.N.
Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65077 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-211 < BLAT> A;Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A;Experimental source: strain K-12, substrain MG1655 R;Alefounder, P.R.; Perham, R.N.
A; Illus: Intercongrees genome sequence of Escherichia COll K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: B65077 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-211 cBLAT> A; Cross-references: GB: AE000375; GB: U00096; NID: g1789282; PIDN: AAC75960.1; PID: g1789290, A; Experimental source: strain K-12, substrain MG1655 A; Alefounder, Ps. Perham, R.N. A) Aincockion: A 272-272
A;Accession: B65077 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Resdiues: 1-211 <blat> A;Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A;Experimental source: strain K-12, substrain MG1655 R;Alefounder, Px; Perham, R.N. M;Alefounder, Px; Perham, R.N.</blat>
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-211 cBLAT> A;Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A;Experimental source: strain K-12, substrain MG1655
A; Modecule Cype: Lond A; Reddues: 1-211 (BLAT> A; Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A; Experimental source: strain K-12, substrain MG1655 R; Alefounder, P. R; Perham, R. N. Modecki, P. 2, 22, 22, 23, 1000
A;Cross-references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75960.1; PID:g1789290, A;Experimental source: strain K-12, substrain MG1655 R;Alefounder, PR:? Perham, R.N. Molymoder, PR:? Perham, R.N. Molymoder, PR: Perham, R.N.
A; Experimental source: strain K-12, substrain MG1655 R; Alefounder, P.R; Perham, R.N. Mol Microbiol 2 222 222 220 2000
N/INCCOMMUNEY, F.K.; FEIMMIN, K.N. MAINTAIN 2 723-723 1000
MOT: MICTORIOT: 3: /23-/32: 1383
A; Title: Identification, molecular cloning and sequence analysis of a gene cluster encod
A:Accession: S04734
A; Molecule type: DNA
A;Residues: 15-211 <ale></ale>
C. Crosser : references: EMBL:X14436; NID:g41417; PIDN:CAA32607.1; PID:g41425
A. General Constant C
A;Morror of a min C;Superfamily: Bscherichia coli hybothetical 23K protein (shm-fha intercenic region)
TOTAL THE TOTAL
Query Match 29.4%; Score 350; DB 1; Length 211; Best Local Similarity 35.7%; Pred. No. 1.6e-24;
Matches 81; Conservative 37; Mismatches 75; Indels 34; Gaps 4;
OY 7 FITGLILGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
Db 5 YPGGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ 64
Db 65 SPWILALVIWGGVAFLLWYGFGAFKTAMSSNIEL98
Qy 127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVPIGGVGAOYG-DTGRWIFAAG 185
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A; Status: preliminary
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                                   probable membrane transport protein STV3222 [imported] - Salmonella enterica subsp. enterica scaled probable membrane transport protein STV3222 [imported] - Salmonella enterica subsp. enterica serovar Typhi
A;NOte: this species has also been called galmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH0874
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Nutne 413, 848-852, 2001
A;Nutne 413, 848-852, 2001
A;Nutne 413, 848-852, 2001
A;Reference number: AB0502; PMID:1167608
A;Reference number: AB0502; PMID:1167608
A;Reference number: AB0502; PMID:1167608
A;Residues: 1-211 <PAR>
A;Residues: 1-211 <PAR>
A;Residues: 1-211 <PAR>
A;Cossion: AH0814
A;Residues: 1-211 <PAR>
A;Cossion: AH0814
A;Generics: GB:AL513382; PIDN:CAD02896.1; PID:g16504149; GSPDB:GN00176
C;Generics: A;Gene: STY3222
C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein EC83794 [imported] - Escherichia coli (strain 0157:H7, substrain RI C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: B91103 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Ritle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gence A; Reference number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ASAEVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLAMEPKRW- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S YFQGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.8%; Score 343; DB 2; Length 211; llarity 35.2%; Pred. No. 6.9e-24; Conservative 37; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.1%; Score 347; DB 2; Length 211; llarity 33.6%; Pred. No. 3e-24; Conservative 42; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA;Residues: 1-211 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local S
Matches 80
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hypothetical protein yggA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: E85948 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: GB:AE005174; NID:g12517455; PIDN:AAG58049.1; GSPDB:GN00145; UWGP:Z42
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360

A; Reference number: Deliminary

A; Molecule type: DNA

A; Residues: 1-205 < KUR>
A; Residues: 1-205 < KUR>
C; Genetics:
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C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
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                                                                                                                                                                                                        ----ASAEVLKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLDVEPKRW-FALG 151
                                                                             98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S YPQGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ
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                                                                                                                                                           127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                                                                                                                                                               187 FAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                  186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL
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65 SPWLLALVTWGGVVFLLWYGFGAFKTAMSSNIEL----
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C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: C97472
R; Godner, B.; Hinhe, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysB family transporter lysB [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AG2690
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                   A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A,Reference number: A97359; PMID:11743194
                 transport protein. (AL357613) [imported] - Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map positTon: circular chromosome
C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
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C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Acesence number: AB2577; PMID:11743193
A,Accession: AG2690
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A,Molecule type: DNA
A,Residues: 1-202 «KUR»
A,Cross-references: GB:AE008688; PIDN:AAL41941.1; PID:g17739308; GSPDB:GN00186
A,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AE007869; PIDN:AAK86732.1; PID:g15155924; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 IQIFFTGLTWGLSLIVAIGAQNAFVLKQGLARSHVFAVCATCAISDALLIMVGVFGFQRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MEIFITGLLIGASLLISIGPONVLVIKOGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWTALAIKLML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-202 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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Matches
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Stover: D83100
R;Stover: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Y.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Tile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: 1-200 <STO>
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <STO>
A;Cross=references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07753.1; GSPDB:GN001
C;Genetics:
A;Gene: PA4365
C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
A,Gene: YPO0918
C,Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transporter PA4365 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSNAAPIVLDIMRWGGIAYLLWF---AVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVATD----TRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQ-Y 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LAVTWLNPHVYLDTFVVLGSLGGQLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKUML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 PDIRPW-FALGAVTASIVWFFALALLAAWLSPWLNRPVAQRIINLFVGGVMGFIAFQLAR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PDAL---GNAAETGP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 IMBIPITGLLIGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: |:|:| | |:::|| | |: |::|| |: |:|| |: | |:|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
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                                                                                                                                    Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 200;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.9%; Score 332; DB 2; Length 20(
ilarity 33.5%; Pred. No. 6.5e-23;
Conservative 42; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 FAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG
                                                                                                                                                                                                                    70;
                                                                                                                                28.1%; Score 335; DB 2; 33.1%; Pred. No. 3.6e-23; ive 44; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| | | | | | | | | | | 65 NPTLLAIARWGGIAFLTWYGLKALLRALR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : :|::| : |||:|:|:|
LLSRSPLLLALVTWGGVAFLMWYGWGALMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 DGVASSATSVTQGRWRILVTL----
                                                                                                                       Query Match
Best Local Similarity 33.1%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches '77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MG 236
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C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C; Accession: AD3411
C; Accession: AD3411
R; DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A; Reference number: AD3252; PMID:11756688
                                      GB:AL123456; NID:g3261586; PIDN:CAA98398.1; PID:g1403469
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C;Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                        A,Gene: Rv1986
C,Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD3411
transporter, lysE family BMEI1274 [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-204 «KUR»
A;Cross-references: GB:AE008917; PIDN:AAL52455.1; PID:g17983261; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : ||:|||: ||| : || : |:
-----CLALTFINPHVYLDTVLLIGSLSARLEGPARAAYGAGAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SGATPVR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ------IAEVLVTCAAPTFINPHVYLDTVVLLGALANEHSDQ-RWLFGLGAV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSGFLLGASLITAIGAQNAFILRQGLLRQHVFILCLICALSDALLISAGVAGLGTLIAQS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VVGFLACFTLIAAIGAQNAFVLRQGIQREHVLPVVALCTVSDIVLIAAGIAGFGALIGAH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 PKLIAFVTLAGAAFLFWYASVAFRRAF--HPEAMQVKSNGAVSLK-----AAAAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR
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                                                                                                                                                                                                                                                                                             Query Match 26.7%; Score 318; DB 2; Length 199; Best Local Similarity 31.1%; Pred. No. 1.2e-21; Matches 70; Conservative 44; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 TASAVWFATLGFGAGRLRGLFTNPGSWRILDGLIAVMMVALGISL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AASLIWPPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
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PRAINVVKFGGAAFLIGYGLLAARRAWRPVALIP----
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A,Residues: 1-199 <COL>
A,Cross-references: GB:Z74025; GB:Al
A,Experimental source: strain H37Rv
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Best Local Similarity 30.2%;
Matches 68; Conservative 4.
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A; Gene: BMEI1274
                                                                                                                                 C, Genetics
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A70500; MUID:98295907; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-201 <COL>
A; Residues: 1-201 <COL>
A; Cross-references: GB:277162; GB:AL123456; NID:g3261606; PIDN:CAB00949.1; PID:g1449286
A; Experimental source: strain H37Rv
C; Genetics:
A; Gene: Rv0488
C; Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
C; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: C70744
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv0488 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 -----IGVVQMCLVVTFLNPHVYLDTVVLIGALANEESDL-RWFFGAGAWAASVVWFA 148
                                                                                                                                                                                                                        136 VDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIĞGVGAQYGDTGRWIFAAGAFAASLIWFP 195
    64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                      --- 108
                                                                                                                                                                            124 TDTRNRVRVBVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TLKVAIGPQNAFVLRQGIRREYVLVIVALCGIADGALIAAGVGGPAALIHAHPNMTLVAR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                 184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.8%; Score 319; DB 2; Length 201; Best Local Similarity 32.4%; Pred. No. 1e-21; Matches 71; Conservative 50; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 LVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML 234
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LysE/YggA family protein VC0481 [imported] - Vibrio cholerae (strain N16961 serogroup O1 C;Species: Vibrio cholerae C;Date: 18-Ang-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001	Qy 193 WFPLVGFGAAALSRPLSSPKVWRW 216
Dodson, R.J.; .; Sellers, F	RESULT 14 D69838
	conserved hypothetical protein yisu - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 C;Accession: D69838
	R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
	Nature 390, 249-256, 1997 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
	Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
	Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ya
Qy 6 IPITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65 : : : :	A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID: 98044033; PMID: 9384377
66 AAPIVLDINKWGGIAYLLWFAVWAKDAMTHKVBAPOIT I EFFEFTVPDDTPLGGSAVATD 125	A.Stratus: Dealminary, A.Stratus: preliminary, nucleic acid sequence not shown; translation not shown A.Molecule type: DA. A.Molecule acid.
65 ONTSLLIGVTLAGILFLCGYGFLSLRAALKPPQASESTANPMAAGRKAV- 113	A;Cross-references: GB:399109; GB:AL009126; NID:g2633260; PIDN:CAB12926.1; PID:g2633422 A;Experimental source: strain 168
OY 128 IRANKVEVSVURQKVWVKEMLMALIVLIWLARVEIGGYGAQYGDTGRWIFAAG 185 Db 114	C;Genetics: A;Gene: yisU C;Superfamily: Bscherichia coli hypothetical 23K protein (sbm-fba intergenic region)
QY 186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWTALAIKL 232 DD 154 TILASFVWFFLLSLGAAKLSTFLSKPRVRQVIDMAVAAMMFIIAFAL 200	Query Match 14.8%; Score 176.5; DB 2; Length 220; Best Local Similarity 22.9%; Pred. No. 1e-08; Matches 53; Conservative 36; Mismatches 99; Indels 43; Gaps 4;
RESULT 13 S57940	QY 4 MEIRITGLLIGASLLLISIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV 60
iggA procein nomolog - Aeromonas nydrophila C;Species: Aeromonas hydrophila C;Accession: 557940 C;Accession: 557940	Qy 61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120 :: : : Dh 78 SVIVORI,DVPRTYMAAGGEIRTI, YMGWV
R;Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B. submitted to the EMBL Data Library, July 1995 A;Reference number: S57938 A;Accession: S57940	121 AVATDTRNRYRVEVSVDKOVEVWVKPMLMAIVLTMLNPNAYLDAFVFIGGVGAQYGDTG 121 AVATDTRNRYRVEVSVDKOVEVWVKPMLMAIVLTMLNPNAYLDAFVFIGGVGAQYGDTG 106TWN-IRPNTSQNEKHTPTPKKQAAFAAAVSLLNPHAILDTIGVIGTSSLQXSGLE
A;Nolecule typelminary A;Nolecule type: DNA A;Residues: 1-211 <swi> A;Cross-references: EMBL:X89469; NID:g899143; PIDN:CAA61655.1; PID:g899146</swi>	QY 179 RWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALA 229 19
Query Match 20.0%; Score 238; DB 2; Length 211; Best Local Similarity 26.6%; Pred. No. 2.5e-14; Matches 58; Conservative 36; Mismatches 70; Indels 54; Gaps 4;	
OY 17 LLLSIGPONVLVIKGGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAAPIVLDIMRW 76 :::	conserved hypothetical integral membrane protein HP0718 - Helicobacter pylori (strain 26 C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000 C;Accession: F64609
QY 77 GGIAYLLWFAVWAAKDAWTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRV 132. : : : :	R,Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
GDTGRWIFAAGAFAASLI :	A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID: 97394467; PMID: 9252185 A; Accession: F64609

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ra, N.; Mogzer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter let, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho mmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Stein, G.; Krogh, S.; Kumano, M.; Kurfie, K.; Lapidus, A.; Lardinois, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Jiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle A. C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, S.; Schroeter, R.; Scoffone, F.; Sckjuuchi, J.; Sekowska, A.; Sero, Shi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, pat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. H.F; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A69580; MUID:98044033; PMID:9384377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UN>
GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12926.1; PID:g2633422
e: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVEVSVDKQRVWV--KPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASLLLSIGPONVLVIKQGIKREGL ---IAVLLVCLISDVFLFIAGTLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%; Score 176.5; DB 2; Length 220; 22.9%; Pred. No. 1e-08; tive 36; Mismatches 99; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLIWPPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALA 229
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   --VWRW 216
                                                              VĽSPWĽARSROGYSKLLILLLVSPCWGW 182
ALSRPLSSPK-
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown

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A,Molecule type: DNA
A,Residues: 1-210 <TOM>
A,Cross-references: GB:AE000585; GB:AE000511; NID:g2313845; PIDN:AAD07771.1; PID:g231384
C,Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)
                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                            91 LPQTFKKKKQVQTPKKLSLKKTLLFTLGVTLLNPQVYLEMVFLIGASALSFNLAQKFVFLA 150
                                                                                                                                                                                                                                                                                           66 AAPIVLDI-MRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                              125 DTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA 184
                                                                                                                                                                                                                                                                                                                    6 IFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                             Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 GAFAASLIWFPL----VGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 210;
                                                                                                            Query Match 14.6%; Score 173.5; DB 2; Best Local Similarity 21.9%; Pred. Nor 1.9e-08; Matches 51; Conservative 48; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 24, 2003, 18:23:47 Job time : 20 secs
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

April 24, 2003, 18:20:37; Search time 11 Seconds Run on:

(without alignments)
889.856 Million cell updates/sec

US-09-105-117K-2 1191 1 MVIMEIFITGLLLGASLLLS......INVVVAVVMTALAIKLMLMG 236 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P94633 corynebacte	P11667 escherichia	Q11154 mycobacteri	_	-	-	P27846 escherichia	P76249 escherichia	P17334 escherichia	O87394 rhizobium m	P75693 escherichia	Q916n7 salmonella	P30589 neurospora	_				P38101 escherichia	P36545 escherichia	026830 methanobact	Q57556 methanococc	Q9zlc0 helicobacte	_	O87656 salmonella	P38102 pseudomonas	Q03131 saccharopol		P18278 acetobacter	P30016 escherichia	P45404 rhizobium m	P12610 escherichia	P12673 salmonella	P27847 escherichia
SUMMARIES	ID	LYSE_CORGL	YGGA_ECOLI	Y488 MYCTU	YJ86 MYCTU	YGGA_AERSA	YGGA_AERHY	RHTC_ECOL1	YEAS_ECOLI	PTCC ECOLI	Y093 RHIME	YAHN_ECOLI	RHTC SALTY	CHS2 NEUCR	CA36 CHICK	RHTC SALTI	DCUA_HELPY	YBIF_SALTY	YFIK_ECOLI		MRAY_METTH	Y091_METJA	DCUA_HELPJ	YFIG_BACSU	FHUB_SALTY	YBF7_PSEAE	ERY1_SACER	CYSZ_SALTI	DHET ACEAC	KUP ECOLI	CCMF RHIME	CYSZ_ECOLI	CYSZ_SALTY	RHTB_ECOLI
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Q8x4v6 escherichia P4633 bacillus su 007708 mycobacteri Q5622 thermus the P28303 escherichia P96792 lactobacill 08706 pseudomonas P75706 escherichia Q5108 deinococcus P15993 escherichia Q91410 salmonella
YGAY ECO57 CSBC BACSU ORN MYCLB NQOE THETH NDOE THETH XYLP LACPE CHPE PSEAE CHPE PSEAE CHPE PSEAE AMOIL BEIRA AROP ECOLI
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: INVOLVED IN THE EFFLUX OF EXCESS OF L-LYSINE. THIS IS
-!SUBCESSARY TO CONTROL THE INTRACELLULAR L-LYSINE LEVEL.
-!-SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                 LYSE OR CGLI262.

Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                                      cellular function: L-
                                                                                                                                                                                                                                       STRAIN=R127;
MEDLINE=97126810; PubMed=8971704;
Vr]ic M.M., Sahh H., Eggeling L.;
M.A new type of transporter with a new type of cellysine export from Corynebacterium glutamicum.";
Mol. Microbiol. 22:815-826(1996).
                                                                         (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                               233 AA.
                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fransport; Transmembrane; Inner membrane.
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InterPro; IPR001123; Ly8E.
InterPro; IRR004777; Ly8_exporter.
                               PRT;
                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND FUNCTION.
                                                           (Rel. 36, Created)
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55
86
164
197
233
25082 M
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                             STANDARD;
                                                                                                        Lysine exporter protein.
                                                                                                                                                                                               NCBI_TaxID=1718;
                                                           .5-JUL-1998
                             CORGL
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RESULT 1
LYSE_CORGL
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POTENTIAL. FSFD9B1ACAD11D13 CRC64;

MM.

233 AA;

SEQUENCE

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TIGR00948; 2a75; 1.

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TIGRFAM8;
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                                    ö
                                                                                                                                                                                                                               61 SNAAPIVLDIMRWGGIAYLLWFAVWAAKDAMTNKVEAPQIIEETEFTVPDDTPLGGSAVA 120
                                                                                                                                         SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                             TDTRNRVRVBVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-KI2 / CS520;

MEDLINE=89113302; PubMed=2546007;

Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;

Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;

Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;

Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;

Identification, molecular cloning and sequence analysis of a gene cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-phosphoglycerate kinase and a putative second glyceraldehyde 3-phosphote dehydrogenase of Escherichia coli.";

Mol. Microbiol. 3:723-721(1989)

-! SUBCELLULAR LOCATION: Integral membrane protein (Probable).

-! SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                           1 MEIFITGLELGASLELSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 60
                                    Gaps
                                                                     4 MEIFITGLLIGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blatthar F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                      181 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 233
                                                                                                                                                                                                                                                                                184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
 Length 233;
                                    Indels
                                    ö
Query Match
98.9%; Score 1178; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.6e-94;
Matches 233; Conservative 0; Mismatches 0;
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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InterPro; IPR001123; LysE.
InterPro; IPR004777; Lys_exporter.
Ffam; PF01810; LysE; 1.
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X14436; CAA32607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein yggA.
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                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGGA OR B2923
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01-OCT-1996
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P11667;
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YGGA_ECOLI
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STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                  7 FITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=9829597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris-
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris-
Cole S.T., Badgmeier K., Gas S., Bary C.E. III. Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Comnor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (
Hornsby T., Jagels K., Krospl A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J. B., Taylor K., Mhitchhead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                       S YPQGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ASAEVMKQGRW-KIIATMLAVTWINPHVYLDTFVVLGSLGGQLDVEPKRW-FALG
                                                                                                                                                                                                                                                                                                                                                                                                                                127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBGELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                 29.4%; Score 350; DB 1; Length 211; 35.7%; Pred. No. 3.6e-23;
                                                                                                                                                                                                                         75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AFAASLIWPPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
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                                                                                                                                         2DAFE27B6A9BE822 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-UUN-2002 (Rel. 41, Last annotation update)
RV0488 OR MT0507 OR MTCY20G9.14.
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                                                                                                                                         23175 MW;
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                                                                                                                                                                                                                         81; Conservative
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                       21
57
88
131
167
199
Hypothetical protein;
TRANSMEM 1 2
                                                                                                                                           211 AA;
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NCBI_TaxID=645;
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15-JUN-2002
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P70775;
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STRAIN-H37Rv;

MEDLINE-98255987; PubMed-9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., A Cole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Badcock K., Jagels K., Krogh A., McLenn J., Woule S., Murphy L., A Hornsby T., Jagels K., Krogh A., McLenn J., Woule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Atter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 -----IGVVQMCLVVTFLNPHVYLDTVVLIGALANEESDL-RWFFGAGAWAASVVWFA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 WGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 VDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAFAASLIWFP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TLKVAIGPQNAFVLRQGIRREYVLVIVALCGIADGALIAAGVGGFAALIHAHPNMTLVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Transmembrane; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 LVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%; Score 319; DB 1; 32.4%; Pred. No. 1.6e-20;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
RV1986 OR MT2040 OR MTCX39.33C.
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rive 50; Mismatches
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InterPro; IPR004777; Lys_exporter.
Fam; PP01810; LysE; 1.
TIGRPAMs; TIGR00948; 2a75; 1.
Hypothetical protein; Transmembran
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                                                                                                                                                                                                                              AE006952; AAK44730.1;
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Nature 393:537-544(1998).
                                                                                                                                                                                                         EMBL; Z77162; CAB00949.1;
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                                                                                                                                                                                                                                                                                      Tuberculist; Rv0488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AA;
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Matches
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[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DoBoy R., Dodson R., Gwinn M.D., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
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                                                                                                                                                                                                                           genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
Aeromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0948; 2a75; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 6 26 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6F330132DDCFD0FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.7%; Score 318; DB 1; 31.1%; Pred, No. 1.9e-20;
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62
88
136
164
108
20775 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z74025; CAA98398.1; -.
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InterPro; IPR004777; Lys e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; Rv1986; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=KI2 / M01655,
MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
[2]
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               "Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate N acythomoserine lactone signal molecules.";
J. Becteriol. 179:5271-5281(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE LYSE/XGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA
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Escherichia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 AVAMLASLVWFYSLAFGAVVLSPWLARSROGYSKLLILLLVSPCWGW 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172DB104473B0B09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 254; DB 1;
; Pred. No. 6.6e-15;
38; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 36, Last sequence update) (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane
                                                                                                                                                                                                                                                                                                                                          EMBL; X89469; CAA61655.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001123; LysE.
InterPro; IPR004777; Lys exporter.
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01810; LysE; 1.
TIGRFAMS; TIGR00948; 2a75; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%;
26.9%;
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Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein;
TRANSMEM 1 21
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P27846;
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(See http://www.isb-Bib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 PIGLALLTWGGVLFLCWFGIRSLRSAWQGQ--------GAALADSPR 104
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                                                                          Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K., Chabara S.R., Williams P., Macintyre S., Stewart G.S.A.B.; Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRi homologs AhyRI and AsaRI and their cognate N.acylhomoserine lactone signal molecules."; Bacteriol. 195:5271-5281(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 NRVRVEVSVDKQRVWVKPML-MAIVLTWINPNAYLDAFVFIGGVGAQYGDTGRWIFAAGA
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 24.5 kDa protein in ahyR-cdpD intergenic region.
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STRAIN=A1;
MEDLINE=97431471; PubMed=9286976;
Swift S., Karlyshev A.V., Fish L., Durant B.L., Winson M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.0%; Score 310; DB 1; Length 206; Best Local Similarity 31.9%; Pred. No. 9.5e-20; Matches 72; Conservative 43; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 MLASLVWFYSLAFGAAALSPWLARGRVQQAIDTIVGLIMLGLALQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 FAASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKL 232
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DIC2C492CDA0179A CRC64;
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InterPro; IPR00477; LysBexporter.
Pfam, PF01810; LysB; 1.
IIGRFAMS; TIGR00948; 2375; 1.
Hypothetical protein; Transmembrane.
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                                                           MEDLINE=97431471; PubMed=9286976;
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01-OCT-1996 (Rel. 34, Last seq
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                                       STRAIN=NCIMB 1102;
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STRAIN=0157:H7 / RIMD 0509952;

STRAIN=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Ruhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12:";
                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Geregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21014935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck R.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The novel transmembrane Escherichia coli proteins involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Irino N., Nakayama K., Nakayama H.;
"The recQ gene of Becherichia coli K12: primary structure and
evidence for SOS regulation.";
Mol. Gen. Genet. 205:298-304(1986).
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                                                                                                         "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
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EMBL; AE000458; AAC76826.1; ALT_FRAME.
EMBL; AE005613; AAG59019.1; ALT_INIT.
EMBL; AP002267; BAB38176.1; -
EMBL; M30198; -; NOT_ANNOTATED_CDS.
PIR; S30713; S30713.
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InterPro; IPR004778; Homoser_Thr_eff.
InterPro; IPR001123; LysE.
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          STRAIN=K12 / MG1655;
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C STRAIN=KI2;

W MEDLINE=97251358; PubMed=9097040;

W ALCOLINE=97251358; PubMed=9097040;

W ALCOLINE=97251358; PubMed=9097040;

W ALCOLINE=97251358; PubMed=9097040;

W ALCOLINE=97251358; PubMed=T., Fujita K., Hakino K., Miki T.,

W Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,

W Mizobuchi K., Mori H., Mori T., Saito N., Sampei G., Seki Y.,

W Mizobuchi K., Moriuchi T., Takemoto K., Wada C.,

W Yasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,

W Amamoto Y., Horiuchi T.;

W A Mamoto Y., Moriuchi T.;

W A Moriuchi T.;

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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                       206 AA; 22474 MW; F64017878CC6D50D CRC64;
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TIGRRAMs; TIGR00949; 2A76; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PIVLDIMRWGGIAYLLW-----FAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EAKSDEPQYGAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 VATDTRNRVRVEVSVDKQRVWVKPMLMAIVIJTWLNPNA---YLDAFVFIGGVGAQYGDTG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 ------OFRALILSLTNPKAILFYVSFFVQFIDVNAPHTGIS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTCC_ECOLI STANDARD;
PT3134; P76201;
P173134; P76212; P77312; P76907;
P173134; P76212; P77312; P76907;
D1-AUG-1990 (Rel. 15, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
PTS system, cellobiose-specific IIC component (BIIC-Cel) (Cellobiose-permase IIC component) (Phosphotransferase enzyme II, C component).
                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels 84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LLGASLLLSI-GPQNVLVIKQGIK---REGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90185127; PubMed=2179047;
Parker L.L., Hall B.G.;
"Characterization and nucleotide sequence of the cryptic cel operon
of Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=97426617; bubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 RWIFAA-----SLIWFPLVGFGA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 FFILAATLELVSFCYLSFLIISGAFVTQYIRTKKKLAKVGNSLIGLMFVGFAA 205
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

8.5%; Score 101; DB 1; Length 212;
Best Local Similarity 22.3%; Pred. No. 0.083;
Matches 52; Conservative 28; Mismatches 69; Indels
                                                                                                                                                                                                                                                   Complete proteome.
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                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                         EMBL; AE000274; AAC74868.1; -.
EMBL; D90823; BAA15593.1; -.
EMBL; D90824; BAA15602.1; -.
                                                                                                                                                                                                                                                                                                                                                                       23200 MW;
                                                                                                                                                                                           BcoGene; EG13505; yeas.
InterPro; IPR001123; LysE.
Pfam; PF01810; LysE; 1.
Hypothetical protein; Trans
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                                                                                                                                                                                                                                                                                                                                    153
188
212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGW -> WL (IN REF. 1).
FVPLLWFFGIHGALALTALDNGIMTP -> LSTALVLRIHA
ACADRTGQRHYDA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                               RES. MICTODIO1. 141:1061-1067(1990).

-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMERANE (THE DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPGFIILSVMGIIAW -> FNSRLYYSFRDGDYCL (IN
                                                                                                            Isono K., Itoh T.,
                                                                                                                                                                                                                                                                                 MEDLINE=91227627; PubMed=2092358; Reizer J., Reizer A., Saier M.H. Jr.; "The cellobiose permease of Escherichia coli consists of three proteins and is homologous to the lactose permease of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane. SIMILARITY: CONTAINS 1 PTS EIIC DOMAIN.
                                                                                                      Alba H., Baba T., Fulita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Mishio Y., Oshima T., Saito I Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 december 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugar transport; Transmembrane;
              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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TIGRPAMS; TIGR00359; Cello pts_IIC; 1.
TIGRPAMS; TIGR00410; pts; 1.
Phosphotransferase system; Sugar trans
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InterPro, IPR003352; PTS_BIIC.
InterPro, IPR004501; Pts.
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                                                                                          MEDLINE=97251357; PubMed=9097039;
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EMBL; M64438; AAA23547.1; -.
EMBL; AE00268; AAC74807.1; -.
EMBL; D90816; BAA15518.1; -.
EMBL; D90817; BAA15526.1; -.
EMBL; D90818; BAA15532.1; -.
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                                                                SEQUENCE FROM N.A.
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147
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YAHN_ECOLI
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           SET TELEFFEE
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                       SVAALLVALFNIGINTLIYLEPVVVANKAQNAIDKEESEED
IANALKF -> TSPHCWSHSSTLASQR (IN REF. 1).
EC3CBFEED6231068 CRC64;
                                                                                                                                                                                                                                   210 WGTNFHQIIMDTISTPLASLGSVVGWAXVIFVPLLWFFGIHGALALTALDNGIMTPWALE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LG------VDLLSNAAPIVLDIMRWGGIAY--LLWPAVM---AAKDAMTNKVEAPQIIE 105
                                                                                                                                                                                                                                                                                                                                                                                 106 ETEPTVPDDTPLGGSAVAT-DTRNRVRVEVSVDKQ-RVWVKPMLMAIVLTWLNPNAYLDA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                     ------- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 FVFIGGVG------AQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPL 208
                                                                                                                                                                 77; Gaps
                                                                                                                                                                                                      8 ITGLLLG---ASLLLSIGPQNVLV----IKQGIKR--EGLIAVLLVCLISDVFLFIAGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeuu A., Kahn D., Kiss B., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puchler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
Sinorhizobium melilot: strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                     DB 1; Length 452;
                                                                                                                                                               95; Indels
       FVLVQP -> LYWYNR (IN REF. 1)
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Powers B.L., Vuyyuru V., Kahn M.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              270 N------IATYQQYGSVBAALAAGKTFHIWAKPM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical transport protein R00093.
                                                                                                              ; Score 93.5; DB
; Pred. No. 0.83;
44; Mismatches
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 MFIPF-----VLVQPILAAITLAAYYMG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
                                                                      48332 MW;
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                                                                                                                  7.9%;
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                                                                      452 AA;
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                                                                                                                                       Best Local Similarity
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CONFLICT
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64 SNAAP-----IVLDIMRWG-GIAYLLWFAVMAAKDAMTNKVEAPQIIEETEFTVP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LLRVLGPAHVWALGVGIVLVGEYMGWNFSVGKGGMIAGLMACWVAGLLYTCVAMIDSEVT 75
                                                                                                                                                            Transport; Transmembrane; Complete proteome.
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H.,
Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 -----VGFLLDTVAGMQGQTGLNQQPFIV---LAIMFLAWLNYRGVLATLTF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland N. Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 QYGDTGRWIFAAGAFAASLIWFPLVGFGAAAL----SRPLSSPKVWRWINVVVAV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 -----NLVITAIAFLAIVALFVSVQFGASAVPLDFSAITSDPLPYGWVGIVASL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 STVAAAGGQYAQAKHIVGPLMAFNVGLFLVMAYTMLBAANAIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0375E164F737AA0A CRC64;
                                                                                                   Pfam; PF00324; aa_permeases; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P75693; P71307;
01-NOV-1997 (Rel. 35, Created)
NOVV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1;
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92.5;
                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
EMBL; AL591782; CAC41480.1; --
INTENTRO; IPRO02293; AA/rel jurmeasel.
Intentro; IPRO04840; Adc permease.
InterPro; IPRO04841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LLLSIGPQNVLVIKQGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50783 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequenc
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein yahN. YAHN OR B0328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                          160
184
221
                                                                                                                                                                                                                                                                                                                                      264
308
                                                                                                                                                            Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Rolmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGV--GAQYGDTGRWIF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --------WYVFFRRGLITDLSNPQTVL-FFISIFSVTLNAETPTWARLMA 165
                                                                                                                                                                                                                                                                                                                                                                                                                       48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AAPIVLDIMRWGGIAYLLWFAVWAAKDAMTNKVBAPQIIEETEP-TVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLLGASLLLSIGP-QNVLVIKQ----GIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEBIPSLIRIVGGAYLLWFAWCSMRRQST-----PQMSTLQQPISAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AAGAFAASLIW--PPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: CONDUCTS THE BFFLUX OF THREONINE (By similarity).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 223;
                                                                                                                                                                                                                                                                                                                                   -> YA (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 22.9%; Pred. No. 0.52;
54; Conservative 33; Mismatches 101; Indels
                                                                                                                                                                                                                                                   Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                    E17F5ABC31EE3F26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
LRLIYEGVTQR
                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      Score 92;
                                                                                                                              EMBL; AE000140; AAC73431.1; -.
EMBL; U7387; AAB18053.1; -.
ECOGENE; EQ13598; YahN.
INCEPPC; IPR004778; Homeser_Thr_eff.
InterPro; IPR001123; LygE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                      24811 MW;
                                                                                                                                                                                                                 Pfam; PF01810; LysE; 1.
TIGREAMS; TIGR00949; 2A76; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Threonine efflux protein. RHTC OR STM01.31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium
                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                 164 1
213 2
223 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602;
                                                                                                                                                                                                                                                 Hypothetical
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
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CONFLICT
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
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the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HLIIBKWAWLHTIIMVGGLYLCWMGYQMLRGALKKQDAAASSPHI------- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | :: | :: | | :: | | 107 ---ELAQSGRS----FLKGLLTMLSNPK----AIIYFGSVFSLFVGD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 QYGDTGRWIFAAGAFA----ASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTAL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 NVGAAARW----GIFALITLETLAWFTVVASLFALPKMRRGYORLAKWIDGFAGALFAGF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNK----VEAPQIIEETEPTVPDDTPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 IMBIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGT--LGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MMMLPPTVAMVHIVALMSPGPDPPFVSQTAVSRSRKEAMMGVLGITCGVMVWAGVALLGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG-----VGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Din A.B., Yarden O.; "The Neurospora crassa chs-2 gene encodes a non-essential chitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Chitin synthase 2 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 250-438 FROM N.A.
MEDLINE=92115692; PubMed=1731323;
Bowen A.R., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J.,
Robbins P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endaryota: Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                               Length 206;
                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 91; DB 1; Length 206;
20.3%; Pred. No. 0.58;
iive 34; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
080477853FC2733F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '944 AA.
                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                    Stydene, SG????; rhtC.
InterPro; IPR004779; Homoser_Thr_eff.
InterPro; IPR01123; LysE.
Pfam; PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95039879; Pubmed=7952169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology 140:2189-2197(1994)
                                                                                                                                  EMBL; AF23324; AAF33433.1; -. EMBL; AE008884; AAL22803.1; -.
                                                                                                                                                                                                                       j; 1.
9: 2A76; 1.
Com
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                                                                                                                                                                                                                                                                                                                           173 P
22498 MW;
                                                                                                                                                                                                                                                             Transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                   50; Conservative
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                                                                                                                                                                                                                                                                                             44
67
150
206 AA;
                                                                                                                                                                                                                                         TIGRFAMS; TIGR00949
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AIKLML 234
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MEDLINE=91035630; PubMed=1977751;
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3137
2042
2379
3137
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A32674; A32674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P12111; 2KNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
2043
2380
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                                                                                                                                                                                                                                                                                                                                                                                             14;
        Proc. Natl. Acad. Sci. U.S.A. 89:519-523 (1992).
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4) - (N-acetyl-beta-D-glucosaminyl)} (N) = UDP + {(1,4) - (N-acetyl-beta-D-glucosaminyl)} (N+1).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
-!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               641 YVCVLLICTQFILSLGNR-----PQGAKRMYLASMIIYAVIMVYTTFATIFIVVRQIQPS 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 -RNRVRV---EVSVDK-ORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TLGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVE----APQI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 QKSDDKPDLELGNNVFTN---LIVSVASTLGLYFVMSFLYLDPWHMFTSAIQYFVLLPSY 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                7 FITGLLLGASLLLSIGPQNVLVIKQGIXREGLIAVLLVCLI-----SDVFLFIAG---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                753 ICTLOIYAFCNTHDVTWGTKGDNVMRTDLGGAIVKGSTVELEMPSDQLDIDSGYDECLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 PAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   865 IGDNFYLRFILW----AVAALAFRALGS-TTFAAINLVSALVEGRVRLRLNMKG 914
                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 I------EBTEPTVPDD---TPLGGSAVATDT-------
                                                                                                                                                                                        EMBL; X77782; CAA54816.1; -.
EMBL; M82951; AAA33582.1; -.
PIR; B45189; B45189.
PIR; P600434; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 89; DB 1; Length 944; 20.3%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                           95; Indels
                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
; F70052AEE083060D CRC64;
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01-FB2-1996 (Rel. 33, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 3(VI) chain precursor.
 Classification of fungal chitin synthases.";
                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 4.4;
54; Mismatches
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                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                             944 AA; 106816 MW;
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                                                                                                                                                                                                                                                                                                                                                                           Local Similaricy
hes 60; Conservative
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                                                                                                                                                                                                                                                                                     617
654
689
733
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                                                                                                                                                                                                                                                                                                                                   893
                                                                                                                                                                                                                                                                            Multigene family.
TRANSMEM 597
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TRANSMEM
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'Complete genome sequence of a multiple drug resistant Salmonella
                     Nature 413:848-852(2001).
--- FUNCTION: CONDUCTS THE EFFLUX OF THREONINE (By similarity).
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-- SIMILARITY: BELONGS TO THE RHT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GSAVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLIWLNPNAYLDAFVFIGGVGAQYGDIG 178
                                                                                                                                                                                                                                                                                                                                                                    --SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPL---G 118
                                                                                                                                                                                                                                                                                                                                                                                                                    TDGSFAFTALDIRNLAALRELLLPNIVGVAQRLI-LLEAPTIVTEVIEVNKKDIVFLIDG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- AQYADTV 492
                                                                                                                                                                                                                                                                                                                                                       GASLLLSIGPQNVLVIKQGIK----REGLIAVLLVCLISDVFLFIAGTLGVDLL----- 63
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                                                                                        INTERRUPTION IN COLLAGENOUS REGION.
INTERRUPTION IN COLLAGENOUS REGION.
INTERRUPTION IN COLLAGENOUS REGION.
                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                 74; Indels 39;
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CELL ATTACHMENT SITE.
CELL ATTACHMENT SITE.
REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                     MW; ECB428578B536357 CRC64;
                                                                   PIBRONECTIN TYPE-III
                                                                                                                                                                                                       (GLCNAC. . . (GLCNAC. . . (GLCNAC. . .
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                (GLCNAC
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCN)
N-LINKED (GLCN)
N-LINKED (GLCN)
N-LINKED (GLCN)
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2155
2161
3083
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3105
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Salmonella typhi
                                                                                                                                      2153
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15-JUN-2002 (
15-JUN-2002 (
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Q8Z3B3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 GGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG-----VGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FLKGLLTNLSNPK----AIIYFGSVFSLFVGD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 QYGDTGRWIFAAGAFA----ASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWTAL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNK---VEAPQIIEETEPTVPDDTPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IMEIFITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGT--LGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HLIIBKMAWLHTIIMVGGGLYLCWMGYQMLRGALKKQDAAASSPHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E9DFCDF4E42D46A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 88; DB 1; Le: 19.9%; Pred. No. 1:1; tive 35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                    Transport; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                            EMBL; AL627278; CAD07933.1; -.
InterPro; IPR004778; Homoser_Thr_eff.
InterPro; IPR001123; LysE.
Pfam; PF01810; LysE; 1.
TIGRPAMS; TIGR0049; 2A76; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22480 MW;
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67
150
206 AA;
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SEQUENCE
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April 24, 2003, 18:21:02 ; Search time 33 Seconds (without alignments)
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                    Run on:
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	1473.549 Million cell updates/sec
Title:	US-09-105-117K-2
Sequence:	1 MVIMEIFITGLLIGASLLLSINVVVAVVMTALAIKLMIMG 236
Scoring table: BLOSUM62	BLOSUM62

Scoring table: BLOSUM62	BLOSUM62
Gapop 10	Gapop 10.0 , Gapext 0.5
Searched:	671580 segs, 206047115 residues
Total number of }	Total number of hits satisfying chosen parameters: 671580
Minimum DB seq le	Minimum DB seq length: 0
Maximum DB seq le	Maximum DB seq length: 2000000000

00000000 ::::S:::: 500 as	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SPTREMBL 21:*
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SPIREMBL_21:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*	4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:*	8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:*	12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_rvirus:*	16: sp_bacteriap:* 17: sp_archeap:*
abase :				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O8rdm4 corvnebacte	O8xxt9 ralstonia s	O8z3w2 salmonella		O8xd10 escherichia						Q8yq87 brucella me	09cki7 pasteurella	O9kun4 vibrio chol	006730 bacillus su	O8rhx9 fusobacteri	_
SUMMARIES	ID	Q8RQM4	Q8XXT9	Q8Z3W2	Q8ZM68	Q8XD10	QBY2F1	O8ZHH6	O9HW36	Q9K4K6	QSUGV8	Q8YG87	Q9CKJ7	Q9KUN4	006730	O8RHX9	025420
	DB	~	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
•	Query Watch Length DB	231	202	211	211	211	212	205	200	204	202	204	226	211	220	207	210
de	Query Match	72.6	29.3	29.1	29.1	28.8	28.2	28.1	27.9	27.6	27.4	25.4	23.9	20.6	14.8	14.7	14.6
	Score	864.5	349	347	346	343	336	335	332	328.5	326.5	302.5	285	245.5	176.5	175.5	173.5
	Result No.	1	7	e	4	S	y	7	œ	σ	10	11	12	13	14	15	. 16

0921c4 helicobacte 099vil staphylococ 097fyl clostridium 092hq4 rickettsia 027538 methanobact 09kfp7 bacillus ha 08y2b8 ralstonia s 09j3a2 pseudomonas 09a37 caulobacter 09k81 bacillus ha 098137 rhizobium l 092ns0 rhizobium l 092ns0 rhizobium l 092ns0 ryiolocter 09km59 vibrio chol 08ujw7 agrobacteri 09km59 vibrio chol 08ujw7 agrobacteri 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol 09km59 vibrio chol	Q9xbr8 zymomonas m Q8y176 ralstonia s Q8xev9 selmonella Q98519 rhizobium 1 Q921y9 rhizobium m Q92u06 rhizobium m
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ALIGNMENTS

RESULT 1 OGRCM4 DC GORQM4 DC GORQM4 DC GORQM4 DT 01-JUN-2002 (TrEMBLrel. 21, Created) DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE 1ysine exporter protein. DE 1ysine exporter protein. COTYDEDACTETIUM efficiens. OC COTYDEDACTETIUM efficiens. OC Actinomycetales; Corynebacterineae; Corynebacteriaceae; COTYDEDACTETIUM. OC Actinomycetales	Query Match 72.6%; Score 864.5; DB 2; Length 231; Best Local Similarity 71.2%; Pred. No. 9.3e-65; Matches 166; Conservative 30; Mismatches 32; Indels 5; Gaps	Qy 4 MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLJSDVFLFIAGTLGVDLL 63	QY 64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAVA 123	OY 124 IDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLAPRAYLDAFVFIGGVGAQYGDTGRWIFA 183 Db 119 VITKQRPRLRITSGTRQVWVRPMLAAIVLTWINPNAYLDAFVFIGGVGAQYGETGRWIFA 178
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184 AGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236

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YGGA OR STM3066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 VRVEVSVDKORVWV-KPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAFA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.3%; Score 349; DB 16; Length 202;
35.1%; Pred. No. 1.2e-21;
ive 40; Mismatches 72; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 SOMDISKAKEADSLPKALLSCLAFTFLNPHVYLDTVFLIGSISÄÖFGDES-WKFGVGÄSÄ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GLLIGASLLLSIGPONVLVIKOGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAAPI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SRLLSALKGD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N. Claudel-Renard C., Cumnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguler P., Thebault P., Malen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Bucker C.A.; Bucker C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
179 AGAFAASLVWFPLVGYGAAALSRPLSSPRVWRWINIGVAVVLTGLAVKLILMG 231
                                                                                                                                                                                                                                                   Probable transmembrane protein.
RSC2024 OR RS03592.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASLIWFPLVGFGAAALSRPL-SSPKVWRWINVVVAVWMTALAIKLMLM 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 AA; 21650 MW; 743460664388E353 CRC64;
                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                            202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|: |:|| |::||:
67 IVDVARYGGAAFILWYGI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible membrane transport protein.
                                                                                                                                            PRT;
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SEQUENCE FROM N.A.
STRAIN-CT18;
MEDLINE,21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AL646067; CAD15726.1; -. InterPro; IPR001123; Ly8E. Pfam; PF01810; Ly8E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.1%;
Matches 80; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 415:497-502(2002).
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                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE 202 AA
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=305;
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                                                                                                                                          OBXXT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
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SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahhia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LSNAAPIVLDIMRWGGIAYLLWPAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 ------ASABVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLAMEPKRW- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 IMBIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 ATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01810; LysE; 1.
TIGRRAMs; TIGR00948; 2a75; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 211 AA; 23220 MW; 64D6FC8FF21F1D0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AA; 23172 MW; 13CB427CABE5A3FC CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Putative LYSE family, amino acid transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 347; DB 16;
Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       EMBL; AL627277; CAD02896.1; -.
InterPro; IPR001123; LybB.
InterPro; IPR004777; LyB_exporter.
Pfam; PF01810; LybB; 1.
IIGRFAMs; TIGR00948; 2a75; 1.
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InterPro; IPR001123; LysE.
InterPro; IPR004777; Lys_exporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.1%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
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InterPro; IPR001123; LysE.
Pfam; PF01810; LysE; 1.
Complete proteome.
SEQUENCE 212 AA; 21896 N
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                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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les 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GMI1000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                 Q8Y2F1
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Q8ZHH6
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli OLS7:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                      LSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAV 122
                                                                                                                                                                                                                                                                                              123 ATDTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWI 181
                                                                      Gaps
                                                                                                                                       3 IMBIRITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S YPQGLALGAAMILPLGPQNAFVWNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                         99 ------ASAEVMKQGRW-KIIATMLAVTWLNPHVYLDTFVVJGSLGGQLAMBPKRW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anatharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                       182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                     DB 16; Length 211;
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                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 28.8%; Score 343; DB 16; I
1 Similarity 35.2%; Pred. No. 4e-21;
80; Conservative 37; Mismatches 76;
                                                                                                                                                                                                                                                  61 LLMQSPWLLALVTWGGVAFLLWYGFGALKTAMSSNLEL-----
29.1%; Score 346; DB lb.
                                           Pred. No. 2.2e-41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, C. 01-MAR-2002 (TrEMBLrel. 20, Lid 01-UUN-2002 (TrEMBLrel. 21, Lid 01-UV, hypothetical protein. YGGA OR Z4260 OR ECS3794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01810; LysE; 1. TIGREAMS; TIGRE00948; 2a75; 1.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                      Local Similarity
hes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=83334;
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                Query Match
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67 APIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDT 126
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                                                                                                              127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
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PAWLTAVRWAGAAFLLAYGARAFRAAW------
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Last annotation update)
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                             212 AA
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01-JUN-2002 (TrEMBLrel, 21, Last
Probable transmembrane protein.
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EMBL; AL646059; CAD13913.1; -.
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01-MAR-2002
01-JUN-2002
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9
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STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDLINE=1470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Braker S., Basham D., Bentley S.D., Brooks K., Cardenor-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.",
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSNAAPIVLDIMRWGGIAYLLWF---AVMAAKDAMTNKVEAPQIIBETEPTVPDDTPLGG 119
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MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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TIGREMB; TIGR00948; 2a75; 1. –
Hypothetical protein; Complete proteome
SEQUENCE 205 AA; 22164 WW; 2965524391474CDA CRC64;
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Last annotation update)
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InterPro; IPR001123; LysE.
InterPro; IPR004777; Lys_exporter.
Putative LysE type translocator
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les 80; Conservative
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01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
Probable transporter.
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                                                        (ersinia pestis.
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Q9HW36;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| | |||||||| | : | | | | 65 NPTLLAIARWGGIAFLTWYGLKALLRALR --------PDAL---GNAAETGP 105
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman S., Chandra G., Chen C.W., Collins Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Indels 34;
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 200;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative membrane transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 332; DB 16; 33.5%; Pred. No. 3.1e-20; ative 42; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AA
                                                                                                                                                                                                                       Pfam; PF01B10; LysE; 1.
PROSITE; PS0195; GLUTAREDOXIN; UNKNOWN_1.
COMPLETE protecome.
SEQUENCE 200 AA: 21144 MM
                                                                                                                                                            EMBL, AE004852; AAG07753.1; -
InterPro; IPR002109; Glutaredoxin.
InterPro; IPR001123; LysE.
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                opportunistic pathogen.
Nature 406:959-964(2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SC07308 OR SC5F8.18.
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1902;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VRVEVSVDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAFAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 A-------VITCLALTWINPHVYLFTVFLLGSVAADRGPL-RWTFGLGAAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GLLIGASILLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAAPI 69
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MEDLINE-21608551; PubMed=11743194; Miler N., Blanchard M.,

MEDLINE-21608551; PubMed=11743194; Miler N., Blanchard M.,

Moodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Cielo C., Slater S.;

"Genome sequence of the plant pathogen and biotechnology agent
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Nester B.W.;
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL, AJ357613; CAB93746.1; -.
InterPro: IPRO01123; LyeE.
Pfam: PF01810: LyeE, WeB:
SEQUENCE 204 AA; 20686 MW; DD1BD686CCC04DA1 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
LySE family transporter.
LYSE OR ATU0927 OR AGR C 1690.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.6%; Score 328.5; DB 1 34.8%; Pred. No. 6.2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                Hopwood D.A.;
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Matches
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Q8UGV8
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SEQUENCE FROM N.A.

STRAIR=16M / ATCC 23456 / BIOTYPE 1;

STRAIR=16M / ATCC 23456 / BIOTYPE 1;

STRAIR=16M / ATCC 23456 / BIOTYPE 1;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 PIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTR 127
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                                                                                                                                                                                                                                                                                                                                                      3 IQIFFTGLTMGLSLIVALGAQNAFVLKQGLARSHVFAVCATCAISDALLIMVGVFGFQRI 62
                                                                                                                                                                                                                                                                                                                    4 MEIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 IDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA
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Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                 27.4%; Score 326.5; DB 16; Length 202; 31.6%; Pred. No. 9.1e-20; ive 42; Mismatches 83; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAIMPALDPIMRYAGAAFLIWYGAKSLYSALRSS-EVLSVAERREAS----
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                                                                                                                                           202 AA; 21943 MW; F43E0FF2AA834D16 CRC64;
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Last annotation update)
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EMBL, AE009566, AAL52455.1, -
InterPro; IPR001123; LysE.
Pema, PP01810, LysE; 1.
Cpan, Proteone.
SEQUENCE 204 AA; 21338 MW; 190CD4DE2R177R0n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
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                        Science 294:2323-2328(2001).
EMBL; AE009057; AAL41941.1; -.
EMBL; AE008023; AAK86732.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, Transporter, LysE family.
Agrobacterium tumefaciens
                                                                                                                                                                                                                                Local Similarity 31.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                Complete proteome. SEQUENCE 202 AA;
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Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
A Azevedo V., Bettero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Entian K.D., Errington J., Fabret C., Ferrari B., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
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Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
MCDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 AAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 IFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 TRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ILLOGFSLGATMIIPIGAONAYVLNÓGİKRHHHLTTAATCGVLDMIFITLGIFGGGALIS
                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium group; Bacillales;
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Last annotation update)
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MEDLINE=98015416; PubMed=9353932;
Roche B., Autret S., Levine A., Vannier F., Medina "A Bacillus subtilis chromosome segment at the 100 degrees position encoding 11 membrane proteins."; Microbiology 143:3309-3312(1997).
                                                                                                                                                                                                                                                                                                              Score 245.5; DB 1
Pred. No. 5.8e-13;
                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
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05,
21,
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TIGR; VC0481; -.
                                                                                                                                                                                              InterPro; IPR001123; LysE. Ffam; PF01010; LysE; 1. Complete proteome. SEQUENCE 211 AA; 22651
                                                                                                                                                                                                                                                                                                                                                             65; Conservative
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                                                                                                                                        Nature 406:477-483(2000)
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Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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01-JUN-2002 (T)
YISU protein.
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                                                                                                                      cholerae.
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006730
ID 00673
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           ---CLALTFLNPHVYLDTVLLIGSLSARLEGPARAAYGAGAA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 IDTRNRVRVEVS-VDKQ-RVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 ---RGNASLQLAKADKQPQTTLHAIIATLLITLLNPHVYLDTVVIIGGIAGTLAFDEKLF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINEL TOR NIG961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Meldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 FLVGALLVSALWFFSLGYGARLLSRFFQRPVTWRILDLVIGVIMWAIAISLIHYG 219
                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVWTALAIKLMLMG
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Last annotation update)
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Last annotation update)
                                                    188 AASLIWFPLVGFGAALSRPLSSPKVWRWINVVVAVVMTALAIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%; Score 285; DB lb; bred, No. 3.1e-16;
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                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PM70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                  "ypothetical protein PM1618."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                       (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                   (TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=747;
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                                                                                                                                                                                                                                                   01-JUN-2001
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Matches
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
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Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K.,
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Weitzenegger T.,
Visat A., Wambut R., Wadler E., Wedler T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H.P., Danchin A.;
"...h.:1;e".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DILLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 AA; 24065 MW; C18C2810F44F9656 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 176.5; DB 16; 22.9%; Pred. No. 3.6e-07; ive 36; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 207 AA
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Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001123; LysE.
InterPro; IPR004777; Lys_exporter.
Pfam; PF01810; LysE; 1.
IIGRFAMs; TIGR00948; 2a75; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Y09476; CAA70650.1;
Z99109; CAB12926.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 22.98
                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
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Matches
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47; Gaps
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                                                                                                                                                                                                                 ---VGSLV 80
                                                                                                                                                                                             4 MEIFITGLLIGASLLLSIGPONVLVIKQGI -- KREGLIAVLLVCLISDVFLFIAGTLGVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLML 234
sequence and analysis of the oral bacterium Fusobacterium
                                                                                                                        14.7%; Score 175.5; DB 16; Length 207; 24.5%; Pred. No. 4.1e-07; ive 35; Mismatches 97; Indels 47;
                                                                    Complete proteome.
SEQUENCE 207 AA; 23192 MW; 5833132210F1A771 CRC64;
                nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
EMBL; AE010488; AAL93960.1; -.
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Matches 58; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
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		Description	C. glutamicum Lvs	C glutamicum prote	C. dlutamicum meta	Corvnebacterium ol	Corvnebacterium th	Escherichia coli V	H. DVlori Burface	H. DVIOTI transmem	C dlutamicum prote	Staphylococcus epi
SUMMARIES	•	ID		AAG93201	AAU71888	AAB79660	AAG64047	AAB01789	AAW20426	AAW20968	AAG89911	ABP39181
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	Query	core Match Length DB	100.0	100.0	98.9	98.9	72.6	29.4	14.3	14.3	11.1	10.0
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WPI; 2001-582269/65
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                                        This sequence is the LysE protein product, a lysine export protein. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                                                                                                                                                                                                                             DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                        100.0%; Score 1191; DB 18; Length 236; 100.0%; Pred. No. 2e-128;
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Ozaki A;
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Ikeda M,
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                    Claim 42; Page 10; 16pp; German.
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07-APR-2000; 2000JP-0159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium;
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NEPSDB; AAH68420.
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Matches 236; Conserv
                                                                                                                                                                   236 AA;
 Corynebacterium
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Tateishi N,
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                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, coryneform bacterium, coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                   Claim 29; SEQ ID NO: 6955; 246pp + Sequence Listing; English
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Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 236; Conservative 0; Mismatches 0; Indels
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23-JUN-2000; 2000US-0606740.
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 234-235; 1737pp; English.
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                                        99DE-1031434.
99DE-1031435.
99DE-1031443.
99DE-1031453.
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                                                                                                     The present invention relates to the isolation of novel Corynebacterium glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP) proteins. The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polynucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria.
                        Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; libid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTTKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 TDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         1 MEIFITGLLIGASLLISIGPONVLVIKOGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
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                                                                                                                                                                                                                                                                                                           Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum MP protein sequence SEQ ID NO:54.
                                                                                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 1178; DB 22; Best Local Similarity 100.0%; Pred. No. 6.1e-127; Matches 233; Conservative 0; Mismatches 0;
                                                                              Disclosure; Page 215-216; 316pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB79660 standard; Protein; 233 AA
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99DE-1030476.
99US-0142101.
99DE-1031415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                proteins of the invention
                                                                                                                                                                                                                                                                              233 AA;
N-PSDB; AAS96098
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08-JUL-1999;
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Haberhauer G;

63

236 231

Best Local Sim Matches 233;

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compounds,

Sequence Query Match

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Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion protein -
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                                                                                                       67 APIVLDIMEWGGIAYLLWFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAVATDT 126
                                    SNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 FITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YFGGLALGAAMILPIGPQNAFVMNQGIRRQYHIMIALLCAISDLVLICAGIFGGSALLMQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; amino acid production; excretion protein gene;
MEIFVTGLLLGASLLLAIGPQNVLVIKQGIKREGITAVIIVCLLSDVVLFTLGTLGVGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 211;
                                                                                                                                                                                                     179 AGAFAASLVWFPLVGYGAAALSRPLSSPRVWRWINIGVAVVLTGLAVKLILMG
                                                                                                                                                                                  184 AGAFAASLIWPPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG
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                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli YggA amino acid excretion protein.
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                                                                                                                                                                                                                                                                                                               AAB01789 standard; Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli; yggA gene; amino aci
amino acid excretion protein.
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99RU-0104431.
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Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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N-PSDB; AAA52691
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Tokhmakova IL;
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                                                                                                                                                                                                                                                                                           124 IDTRNRVRVBVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a gene from a high temperature-resistant coryneform microbe that encodes a heat-resistant lysin blosynthetic enzyme enzyme has aspartate-semialdehyde dehydrogenase activity and can be used for growing amino acid-producing microbes. The present amino acid sequence corresponds to an enzyme of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEIFITGLILGASLLISIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 63
                                                                                                                                               63
                                                                                                                                                                      1 MEIFITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL 60
                                                                                                                                             4 MEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe -
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                                                                        Length 233;
                                                                                                           Indels
cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat-resistant; lysin biosynthesis; enzyme; coryneform;
aspartate-semialdehyde dehydrogenase; lysE.
                                                                                            Pred. No. 6.1e-127;
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                                                                        DB 22;
                                                                     98.9%; Score 1178; D
llarity 100.0%; Pred. No. 6.1
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG64047 standard; Protein; 231
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vitamins,
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N-PSDB; AAH45375.
                                                                                          Similarity
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                                    233 AA;
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AAG64047

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protein, having five transmembrane regions.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORP of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORP were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts.
                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
127 RNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG-DTGRWIFAAG 185
                    ----ASAEVWKQGRW-KIIATMLAVTWLNPHVYLDTFVVLGSLGGQLDVEPKRW-FALG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence shows a Helicobacter pylori surface membrane
                                                                                         186 AFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWMTALAIKL
                                                                                                                                                                                                                                                                                                          H. pylori surface membrane protein 33986087.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 73; Page 604; 1481pp; English.
                                                                                                                                                                                              AAW20426 standard; Protein; 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0630405.
                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                            Cytoplasmic; vaccine;
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N-PSDB; AAT67601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1996;
07-JUN-1995;
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membrane spanning regions.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori [11fe cycle activators or inhibitors.]

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be inslated from H. pylori by PCR amplification for recombinant polypeptide
                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic, vaccine, prevention, treatment; infection, envelope, identification, binding compound; bacterium; life cycle, activator, bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a H. pylori protein likely to contain five
 66 AAPIVLDI-MRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT
                                                                125 DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA
                                                                                                                                                     | :|: | :| | :: | 121 GTLSAAFSWLLLCTMSLRYG----SKLLNNQKIFMGVNLFVTAIMGTLSVTL 199
                                                                                                                                GAFAASLIWFPL-----VGFGAAALSRPLSSPKVWRWINVVVAVVWIALAIKL 232
                                                                                                                                                                                                                                                                                                                                                     H. pylori transmembrane protein, hp2p10625orf14.
                               63 AKNLYLSLFLNLFGAVFTGFYAFLALK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 73; Page 1359; 1481pp; English.
                                                                                                                                                                                                                                                  AAW20968 standard; Protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US09122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0630405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berglindh OT,
                                                                                                                                                                                                                                                                                                                    21-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9640893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis.
                                                                                                                                                                                                                                                                                     AAW20968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                185
                                                                                                                                                                                                                 RESULT 8
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Score 170.5; DB 18; Length 215; Pred. No. 3.7e-11;

14.3%; 21.5%;

Query Match Best Local Similarity

2

43;

DB 18; Length 210;

6 IRITGLLIGASLLLSIGPQNVLVIKQGIKREGLIAVLLVÇLISDVFLFIAGTLGVDLLSN 65

14.3%; Score 170.5; DB 18; Length ilarity 21.5%; Pred. No. 3.6e-11; Conservative 48; Mismatches 92; Indels

Best_Local Similarity Matches 50; Conserv

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Query Match

226 AA;

Sequence

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us-09-105-117k-2.rag

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Where: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                            96 LPQTFKKKQVQVPPKKLSLKKTLLFTLGVTLLNPQVYLEMVFLIGASAMSFNLVQKFVFLA 155
                                                                                                       66 AAPIVLDI-MRWGGIAYLLWFAVMAAKDAMTNKVBAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                        .25 DTRNRVRVBVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA 184
                                                      6 IPITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVPLFIAGTLGVDLLSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                 Claim 17; SEQ ID NO: 3665; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                             185 GAFAASLIWFPL-----VGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKL
 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C glutamicum protein fragment SEQ ID NO: 3665.
 Mismatches
                                                                                                                           | : | : : | : : | | 68 AKNLYLSLFINLFGAVFTGFYAFLALK------
                                                                                                                                                                                                                                                                                                                                                                   AAG89911 standard; Protein; 226 AA
48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999;
07-APR-2000;
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Tateishi N,
 20;
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37860. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                             STYPAILNILQLVGGGYLTWMGIGAVRSWWTKR-----STQQAAADSQAVENTLVTA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                        65 NAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                              Gaps
                                                             64
                                                                                         64
                                                                              181 IFAAGAP--AASLIWPPLVGFGAAALSRPLSS--PKVWRWINVVVAVVMTALAIKLMLMG
                                                                                                                                                                                                                                                                      7 FITGLLLGASLLLSIGPONVLVIKQGIK--REGLIAVLLVCLISDVFLFIAGTLGVDLLS
                                                                                                                                                                                      DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWL-NPNAYLDAFVFIGGVGAQY--GDTG-RW
                                                                                                                                                                                                                   117 TAAS-----VGVWPAIRSGIATNLSNPKAVL----FFGSVFAQFVRPDMGIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4026
                              39;
 22; Length 226;
                              Indels
                              98;
; Score 132.5; DB 2; Pred. No. 9.3e-07; 45; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID 4026; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                              ABP39181 standard; Protein; 173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
11.1%;
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97US-064964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-381255/41
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              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1998;
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002
                              58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
 Query Match
Best Local
                              Matches
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Claim 1; Page 15-16; 24pp; English.
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ID AAY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAB11630-B11688 represent proteins from Agrobacterium vitis
which elicit a hypersensitivity response (HR) in a plant. The invention
also relates to nucleotide sequences (AAA61501-A61524) encoding the A.
vitis HR elicitor proteins. The HR is a rapid, localised necrosis that
is associated with the active defence of plants against many pathogens,
and occurs when a pathogenic organism interacts with a nonhost plant
(i.e. one in which intracellular bacterial growth and disease development
of on ot occur). Like other HR elicitors, the A. vitis elicitor functions
in non-host plants by causing a rapid hypersensitive response that
results in walling-off and killing of the pathogen. On grape plants, the
A. vitis elicitor induces a restricted necrosis of tissues, resulting in
CC A. vitis elicitor induces a restricted necrosis of tissues, resulting in
CC the death of plant cells and induction of pathogen resistance. A. vitis
CH elicitor proteins, in non-infectious form, are used to treat plants or
thair seeds to impart resistance to disease, such as those caused by
fungi, bacteria or viruses; and to enhance growth, e.g., to increase
                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                                                                                                                                                            EAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPN 158
                                                                                                                                                          159 AYLDAFVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWIN 218
                                                                  39 IAVLLVCLISDVFLFIAGTLGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKV 98
                                                                                                                                   ------MSAKKQ-----ILFALSVSLLNPH
                                                                                                                                                                                                                                                                                                                                                                                                               Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer;
                                                                                                                                                                                                                                                                                                                                                                                   A. vitis hypersensitive response elicitor protein, SEQ ID NO:9.
                             39;
 DB 23; Length 173;
                           Indels
    .5;
2e-05;
83;
                          32; Mismatches
10.0%; Score 119.5; 23.0%; Pred. No. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                         stress resistance; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 85-86; 157pp; English,
                                                                                                                                                                                                                                                                                                      AAB11637 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang H;
                                                                                                                                                                                                            219 VV--VAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                             151 KVSSVIVIIVGLILKKNIVG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US26079.
            Best Local Similarity 23.0%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypersensitive response
                                                                                                                                                                                                                                                                                                                                                          23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herlache TC,
                                                                                                                                61 EKPSNIERIEP-----
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N-PSDB; AAA61502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium vitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200028056-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                 AAB11637;
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 Query Match
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                                                                                                                                                                                                                                                                              RESULT 11
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yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 VDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGG 119
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 FITGLILGASL----LLSIGPQNVLVIKQGI----KREGLIAVLLVCLISDVFLFIAGTLG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 PLSHQLLW----GLFISLSHLLWF------ASVSTFLSNPAIRTVVLRRQRLFNILLIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SAVAIDIRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQY--GDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 -----TSIFVISLYTQFIGKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-----RWIFAAGAF--AASLIWFPLVGFGAAALSRPLSSPKV-----WRWINVVVAV
                                                                                                                                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                              Length 229;
                                                                                                                                                                                                                                                                                                                                           Match 9.6%; Score 114.5; DB 21; Length Local Similarity 23.3%; Pred. No. 0.00011; les 59; Conservative 42; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belareva AV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-threonine synthesis; rhtC;
L-leucine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. coli L-threonine resistance protein, RhtC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY99598 standard; Protein; 206 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0125406,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-threonine resistance;
L-homoserine; L-valine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 VLASLGAILFTAG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 VMTALAIKLMLMG 236
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N-PSDB; AAA48443.
                                                                                                                                                                                                                                                                                       229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1013765-A1
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                                                                                                                                                                                                                                                                                       Sequence
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                                 L-threonine
   present sequence is the L-threonine resistance protein, RhtB, from
                                                                                                                          bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 VDLLSNAAPIVLDIMRW-----GGIAYLLWFAVMAAKDAMTNK---VEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 TVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AIIYFGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IMBIFITGLLLGASLLLSIGPQNVLVIKQGIKR---EGLIAVLLVCLISDVFLFIAGTLG 59
                           Escherichia coll. The coding sequence may be used to impart L-threor resistance on E. coll bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHL-----IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli YeaS amino acid excretion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.8%; Score 105; DB 21
20.4%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB01787 standard; Protein; 212 AA.
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amino acid excretion protein;
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99RU-0104431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 20.4%
tes 51; Conservative
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N&PSDB; AAA52689.
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                                                                                                                                                                                                                                                                                                                                                                                                  206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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The present sequence is the YeaS amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, valine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                       ---EAKSDEPQYGAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FKRALILSLTNPKAILFYVSFFVQFIDVNAPHTGIS 152
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                           12 LLGASLLLSI-GPQNVLVIKQGIK---REGLIAVLLVCLISDVFLFIAGTLGVDLLSNAA 67
                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                            PIVLDIMRWGGIAYLLW-----PAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSA
                                                                                                                                                                                                                                                                                                                                                                                                                      122 VATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNA---YLDAFVFIGGVGAQYGDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 FFILAATLELVSFCYLSFLIISGAFVTQYIRTKKKLAKVGNSLIGLMFVGFAA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GAFAA------SLIWFPLVGFGA 201
                                                                                                                                                                                                                              Length 212;
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                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS,
                                                                                                                                                                                                                            Score 101; DB 21;
Pred. No. 0.0036;
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                 8.5%; Scor.
22.3%; Pred. No. o...
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; osteopathic; neuroprotectant
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PILFNIVRYLGAFYLLYLGSKILYATLKGKNS------
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                                 Claim 1; Page 21; 29pp; English.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                            52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes.
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS59589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 RWIFAA-----
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                              Matches
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Carr GJ;

Trawick JD,

'n Wall

Zyskind JW,

Ohlsen KL,

Xu HH;

2000US-242578P

of .

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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 10183; 511pp; English.
                                                             27-NOV-2000; 2000US-253625P
22-DEC-2000; 2000US-257931P
                                                                                                     16-FEB-2001; 2001US-269308P
                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                             WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                    N-PSDB; AAS52449.
                        26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                               Haselbeck R,
                                                                                                                                                                                                      Yamamoto RT,
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                                                                    Sequences ANDSIDS_ANDSORY LEPPENDENT EXPONDENCELLUM actues Immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyalitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies placific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes proteins. The antibodies may also be used as daynestic agents for determining P. acnes presence, for example, by carryme linked immunosorbent assay (ELISA).

Note: The sequence data for this parent did not form part of the printed of the user in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the view in the v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 NRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRW---IFAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GIAYL-LWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT--DTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 SLGLAAFGGAFLTLLLVIMVARQRQT--MTAGTLI------LTGTAVSALLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LLVCLISDVFLFIAGTLGVDLLSN--AAPIVLD------IMRWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 GAFA-----ASLIWFPLVG-FGAAALSRPLSSPKVWRWINVVVAVVMTALAI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVIMBIFITGLLLGASLLLSIGPQNV-----LVIKQGIKREGLIAV----
                                                         Sequences AAU39105-AAU68017 represent Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.3%; Pred. No. 0.04;
Matches 69; Conservative 39; Mismatches
                  Example 1; SEQ ID No 19424; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. coli cellular proliferation protein #171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU34590 standard; Protein; 452 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000; 2000US-191078P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 AA;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella promeumoniae, Pseudomonas aeruginosa and Enterococcus facealia. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins, programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 ETEPTVPDDTPLGGSAVAT-DTRNRVRVEVSVDKQ-RVWVKPMLMAIVLTWLNPNAYLDA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 ISGIIIGLVVÄEMFTFIVRRÄWVIKLPDSVPASVSRSFSALIPGFIILSVMGIIAWALNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 LG------VDLLSNAAPIVLDIMRWGGIAY--LLWFAVM---AAKDAMTNKVEAPQIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 WGINFHQIIMDTISTPLASLGSVVGWAYVIFVPLLWPFGIHGALALTALDNGIMTPWALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 N------IÀTYQQYGSVEAALAAGKTFHIWAKPM------LDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ITGLLLG---ASLLLSIGPONVLV----IKQGIKR--EGLIAVLLVCLISDVFLFIAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 93.5; DB 22;
19.4%; Pred. No. 0.073;
ive 44; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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357 MFIPF----VLVQPILAAITLAAYYMG 379
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Job time : 38 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.9%
Best Local Similarity 19.4%
Matches 52; Conservative
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Sequence 13983, A Sequence 4, Appli Sequence 75, Appl Sequence 5239, Ap Sequence 1277, Ap Sequence 56, Appl Sequence 25,

App App App App App App App App App

Sequence Sequence Sequence Sequence

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Sequence 252,

Sequence

Sequence Sequence Sequence

Sequence 252, Sequence 252, Sequence 252,

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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1 MVIMBIFITGLLIGASILLISIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTIGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVIMBIPITGLLIGASLLISIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLPIAGTLGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1191; DB 9; Length 236; 100.0%; Pred. No. 3.4e-112; ive 0; Mismatches 0; Indels 0
           US-10-217-096-4

US-09-19-497-75

US-09-925-301-1277

US-09-925-301-1277

US-09-925-301-1277

US-09-925-301-1277

US-09-928-626-4443

US-10-028-072-252

US-10-121-049-252

US-10-121-049-252

US-10-121-049-252

US-10-131-952

US-10-140-474-252

US-10-140-474-252

US-10-140-474-252

US-10-140-474-252

US-10-140-474-252

US-10-140-474-252

US-10-140-141-252

US-10-142-419-252

US-10-142-419-252

US-10-142-419-252

US-10-142-413-252
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APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENCH, AKIHIRO
APPLICANT: SENCH, AKIHIRO
APPLICANT: SENCH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PETENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-09-738-626-6955
Sequence 6955, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NARAGAMA, SATOSHI

    TYPE: PRT
    ORGANISM: Corynebacterium glutamicum
US-09-738-626-6955

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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
KEEDA, MASATO
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Best Local Similarity 100.(
Matches 236; Conservative
SEQ ID NO 6955
LENGTH: 236
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Appli
Sequence 2, Appli
Sequence 11980, A
Sequence 10104, A
Sequence 20, Appl
Sequence 50, Appl
Sequence 5024, Ap
Sequence 5086, Ap
Sequence 5086, Ap
                                                                                                                          (without alignments)
1112.390 Million cell updates/sec
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                                                                                                                                                                                                1 MVIMBIFITGLILGASLILS.....INVVVAVVMTALAIKLMIMG
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/Purl NEW_PUB.pep:*
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                                                                                                      April 24, 2003, 18:23:28 ; Search time 17 Seconds
           GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-746-660A-52
US-09-738-626-3665
US-09-738-626-6998
US-09-738-626-6356
US-09-738-626-6356
US-09-738-626-6356
US-09-738-626-6356
US-09-738-626-636
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US-09-847-332-2

US-09-815-242-11980

US-09-815-242-10104

US-09-738-626-4488

US-09-976-059-20
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US-09-738-626-3783
US-09-738-626-5086
US-09-738-626-5086
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 301932 seqs, 80129803 residues
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                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1191
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Match Length
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0;

61 DLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS 120

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1178 132.5 93.5 91.5 91.5 91.5 89.5 89.5

84.5 86 86

83 82

Score

Result

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125 DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWL-NPNAYLDAFVFIGGVGAQY--GDTG-RW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 IFAAGAF--AASLIWFPLVGFGAAALSRPLSS--PKVWRWINVVVAVVMTALAIKLMLMG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 NAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FITGLILGASLLLSIGPONVLVIKOGIK--REGLIAVLLVCLISDVFLFIAGTLGVDLLS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FLALFLVWIAAIASPGPDLFQIIRLSAKNRRDGVLTAVGIMVGNSIWI-İASLLGLSALI 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 132.5; DB 9
; Pred. No. 1.2e-05;
45; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                             Sequence 3665, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANAMASHI, MIXIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3665
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Ku, H. Howard
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TATEISHI, NAOKO
SENOH, AKIHIRO
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Best Local Similarity
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US-09-815-242-10183
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                                                                             121 AVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRW 180
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61 DLLSNAAPIVLDIMRWGGIAYLLWFAVWAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGS
                                                                                                                  121 AVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRW
                                                                                                                                                                                181 IFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTALAIKLMLMG 236
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APPLICANT: Adjust, Obnat
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: BYUNG-JOON
TITLE OF INVENTION: ORTHEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY FROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION WUMBER: US/09/746,660A
CURRENT APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/142101
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-03
PRIOR PILING DATE: 1999-07-03
PRIOR PILING DATE: 1999-07-03
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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US-09-746-660A-52
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Schroder, Hartwig
Zelder, Oskar
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SOFTWARE: Patentin Vers. 2.0
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Best Local Similarity 100.
Matches 233; Conservative
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212 VPTPTSDLAIVSKGIDLKGSMKIILSV-----PGLLALVL-----FASFNNLIGG 256
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                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                               163 -AIGFLG-----MEITLW----ICLGLSLVALLHLLPIRVDEPEIITQEDAQPTVSDDS 211
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                                                                                                                                                                                                                           6 IFITGLLLGASL--LLSIGPQNVLVI----KQGIKREGLIAVL--LVCLISDVFLFIAGT 57
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                                                                                                                                                                                                                                                                                                                                                                                                          115 --TPLGGSAVAT---DTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGG
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                                                                                                                                           Length 459;
                                                                                                                                                                                      84; Indels
                                                                                                                        29; Mismatches
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24.8%; Pred. No. 0.
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CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
                               ; LENGTH: 459
; TYPE: PRT
; Corynebacterium glutamicum
US-09-738-626-6998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6356, Application US/09738626
Publication No. US20020197605A1
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ANDO, SEIKO
                                                                                                                                      Query Match
Best Local Similarity 23.4*
Matches 61; Conservative
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SEQ ID NO 6356
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SENOH, AKIHIRO
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Matches 51; Conserved
         SEQ ID NO 6998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
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                                                         PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PSECS FOR WINDOWS VERSION 4.0
SEQ ID NO 10183
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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Publication No. US20020197605A1
2000-03-21
NUMBER: 60/206,848
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                               IOR FILING DATE: 2000-05-23
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APPLICANT: NAKAGAWA, SATOSHI
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TATEISHI, NAOKO
SENOH, AKIHIRO
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112 MLGAALFYGDVVITPAISVLSATEGLTVISPSFER-FILPVSLAVLIA---IFAIQPLGT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----WALRLIVA-----EP---FQAFVLLGAVVLTVTGAEA 235
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                                                                                                                                                                                                                                                                                                                                                                                           12 LLGASLL-----LSI--GPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 QYGDTGRWIFAAGAFAASLIWFPLV------GFGAAALSRPLS-----SPKVWR
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                                                                                                                                                                                                                                                                                        7.6%; Score 91; DB 9; Length 624; 20.7%; Pred. No. 0.7;
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APPLICANT: ALCOSHIN, VLADIMIR VENYAMIOVICH
APPLICANT: BELAREOVA, ALL VALENTINOVNA
APPLICANT: TOKHMAKOVA, ILINA LVOVNA
TITLE OF INVENTION: BNA CODING FOR PROTEIN WHICH CONFERS ON
TITLE OF INVENTION: POR PRODICTING THE OF INVENTION: POR PRODICTING THE OF INVENTION: FOR PRODICTING TO LO-HOMORY
FILE DEPENDENT....
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                                                                                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/927,395
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/396,357
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: RU98118425
PRIOR FILING DATE: 1998-10-13
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                                00/280988
                                                                                                                                                                                                                Corynebacterium glutamicum
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Patent No. US20020058314A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 WINVVVAVVMTALAIKLMLMG 236
PRIOR FILING DATE: 2000-04-07
PRIOR PELLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
LENGTH: 624
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                                                                                                                                                                                                                                                                                                                                           54; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 205
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US-09-927-395-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : | ||:
168 EKVGKAFGPIM-----
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 54; Conserv
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                                                                                                                                                                                        TYPE: PRT
ORGANISM:
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                                -- 324
                                                                          148 MAIVLTWINPNAYLDAFVFIG-----GVGAQYGDTGRWIFAA-GAFAASLIWFPLVGF 199
                                                                                                                                  -----GA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 MAIVLTWINPNAYLDAFVFIG-----GVGAQYGDTGRWIFAA-GAFAASLIWFPLVGF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 VIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDLLSNAAPIVLDIMRWGGIAYLLWFAV 87
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FARWICK, Mike
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE dctA GENE
FILE REFERENCE: 20230J WD 199
CURRENT APPLICATION NUMBER: US/09/951,7g0
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                325 -AIYLTM-----ASIPIADAMNMPMSLGEQVGLLVFMILASKGAAGVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 -AIYLTM-----ASIFIADAMNMPMSLGEQVGLLVFMIIASKGAAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
286 SSSESALPNLMRKMEHIGVAKPTVGIVVPTGYSFNLDGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 SSSESALPNLMRKMEHIGVAKPTVGIVVPTGYSFNLDGT
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Best Local Similarity 24.8%; Pred. No. 0.4;
Matches 51; Conservative 29; Mismatches
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                | | | | : ||| |:: ::|:| : 369 GIATLAAGLSSHRPELLHGVDVIVGI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Corynebacterium glutamicum
US-09-951-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Application US/09738626
o. US20020197605A1
                                                                                                                                                                                  200 GAAALSRPLSS--PKVWRWINVVVAV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 GIATLAAGLSSHRPELLHGVDVIVGI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 GAAALSRPLSS--PKVWRWINVVVAV 223
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
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TATEISHI, NAOKO
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Publication No. US200
GENERAL INFORMATION:
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PPLICANT PPLICANT --MTN 96

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60 VDLLSNAAPIVLDIMR-W-----GGIAYLLW-----FAVMAAKDAMTNKVEAPQIIEE 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 IGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AG------AATALAGPIAF---VGLVAPHLARLLAGPD-QRWILPFSALIAA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: IDENTIFY. 011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEC ID NOS: 14110
SEC ID NO 11980
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FILING DATE: 2000-11-27
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US-09-815-242-11980
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Zyskind, Judith W.
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ORGANISM:
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APPLICANT: ALCOSHIN, VLADIMIR VENYAMIQVICH
APPLICANT: BLEAREOVA, ALL VALENTINOVNA
APPLICANT: BLEAREOVA, ILI VALENTINOVNA
TITLE OF INVENTION: DAC CODING FOR PROTEIN WHICH CONFERS ON BACTERIUM
TITLE OF INVENTION: ESCHERICHIA COLI RESISTANCE TO LO-HOMOSERINE AND METHOD
FILE REFERENCE: 0010-1039-0
CURRENT APPLICATION NUMBER: US/09/847,392
CURRENT FILING DATE: 2001-05-03
  96 NLW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVF--LFIAGTLGVD 61
                                                                        97 KVEA-----PQIIBETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVK 144
                                                                                                             122 PKSIVFLAALFPQFIMPQQPQLMQYIVLGVTIVVDIIVMIGYATLAQRIALWIK 176
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ITITLE OF INVENTION: Identification of Essential Genes in ITITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 89.5; DB 10; Best Local Similarity 20.6%; Pred. No. 0.23; Matches 36; Conservative 25; Mismatches 79;
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LIVSHITS, VITALY ARKADIEVICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDA-
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/396,357
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1998-10-13
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PRIOR FILING DATE: 2000-03-21
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Patent No. US20020102670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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US-09-847-392-2
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Matches
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-----LTWL--LACLAVMLL 253

Gaps

Indels

DB 10; Length 340;

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54 IAGTLGVDLLSNAAPIVLDIMRWGG----IAYLLWFAVMAAKDAMTNKVEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 LAGTVNWDLLAVAA-AVLAILAWERDRPLLAGVLIGLGTAAK-----LFPLVL---- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 TVPDDTPLGGSAVATDTRNRVR--VEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 GGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVIMEIFITGLLL-----GASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 ------LGPVLLLCLRQRRMRRFARVAAGAAGAW---LLVNLPVVALQPDGWMEFWRFN
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Best Local Similarity 20.6%; Pred. No. 1.8;
Matches 50; Conservative 37; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AGRGAEFGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAI 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 GIAVALEFTGPLAVALFSSRRPVDFVWV---VLAVLGLWF1LPLGQDVSHVDLTGCALAL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 NPNAYLDAFVFIG-GVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVW 214
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                                                                                                                                                                                                                                                            Length 295;
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                        Query Match 7.2%; Score 86; DB 10; Best Local Similarity 21.9%; Pred. No. 0.82; Matches 58; Conservative 39; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GSAVATDTRNRVRVEVSVDKQR----VWVKPMLMAIVLTW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 RLPLLFYGVSL-----GGMNYLFYLSIQ------
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-6
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 10104
LENGTH: 295
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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PRIOR APPLICATION NUMBER: JP 00/280989
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4488, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                       ; ORGANISM: Escherichia coli
US-09-815-242-10104
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Gaps

85;

Length 415; 71; Indels ---LWFALDGLG-----LHMPAVNAVALATFGVLLAG 283

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NAME/KEY: misc_feature
LOCATION: (1)...(1)
OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that
OTHER INFORMATION: the biosynthesized protein will have a formylmethionine residue
OTHER INFORMATION: at this position
                                                                                                                                                                                                                                                                                                                                                               ---- DKKYDF 192
                                                                                                                                                                                                                                                                             ----GKIWTSPTAFFIMLFFGLQSMNAYIQMGWL-PK 234
                                                                                                                                                                                                                                                                                                                                     --ASLIWFPLVGFGAAAL 204
63
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US-05-976-059-20
Sequence 20, Application US/09976059
Fatent No. US20020164747A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Eargeoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REPRENCES: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
                                6 IFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLG--VDLL
                                                                                                         --AAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTV
                                                                                                                                                                 157 FSGSNAWRWAIFIWALPAVLQVAIW----LPMWW-----
                                                                                                                                                                                                                        PDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVL-
                                                                                                                                                                                                                                                                                                                                  159 AYLDAFVFIGGVGAQYGDTGRWIFA----AGAFA---
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                          193 PAETVKSGST-----
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                                                                                                            64 ---SN-
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59 GVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.0%; Score 83; DB 10; Length 295; Best Local Similarity 20.4%; Pred. No. 1.6; Matches 54; Conservative 44; Mismatches 87; Indels
                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GSAVATDTRNRVRVEVSVDKORV----WVKPMLMAIVLTW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 14000, Application US/09815242 atent No. US20020061569A1
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REING APPLICATION NUMBER: 60/191,078
REING APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 RW----INVVVAVVMTALAIKLMLM 235
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                                                                    F. Haselbeck, Robert
F. Ohlsen, Kari L.
F. Zyskind, Judith W.
F. Wall, Daniel
F. Trawick, John D.
F. Carr, Grant J.
                                                                                                                                                                                                                                        amamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14000
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RESULT 2
US-09-396-357-2
Sequence 2, Application US/09396357
Patent No. 6303348
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIVSHITS, VITALY ARKADIEVICH
APPLICANT: ZAKATAEVA, NATALYA PAVLOVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 KVSSVIVIIVGLIILKNIVG 170
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Query Match
Best Local Similarity
Matches 46; Conserv
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2, Appli
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Sequence 2, Appli
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462.921 Million cell updates/sec
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                                                                                                          April 24, 2003, 18:21:48 ; Search time 15 Seconds
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. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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               GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-439-009A-2
US-09-105-390-64
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US-08-793-044-3
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US-08-112-208C-9
US-08-248-819A-9
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Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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US-08-471-058-13
US-08-337-646A-9
US-08-856-531-9
US-08-856-034-9
US-08-471-057-13
US-08-477-048-7
US-08-277-326-9
PCT-US95-04600-25
US-08-46-326A-40
US-09-045-631-2
US-09-041-886-25
US-09-041-886-25
US-08-463-0928-6
US-08-463-0978-6
US-08-463-0978-6
US-08-463-0978-6
US-08-463-179A-6
US-08-463-179A-6
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Sequence 4026, Application US/09134001C

Radern No. 6380370

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: GTC-00.

CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 IAVLLVCLISDVFLFIAGTLGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKV 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 119.5; DB 4 23.0%; Pred. No. 3.5e-06; ative 32; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4026
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176 DTGR-----WIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVVMTAL 228
                                                           | : | : | : | |: | 155 SNGNIHMKSEVALFAFSVVVVICLWFLFCVFIFQYIKLLFSRPRFKAIFDYIVGFVLIGL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AAPIVLDI-----MRWGGIAYLLW-----FAVMAAKDAMTNKVE-----APQIIEETEPT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||:|
53 SAPVVFVFPGQGAQWAGMAGELLGESRVFA--AAMDACARAFEPVTDWTLAQVLDSFEQS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 VPDDTFLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAI----VLTWLNPNAYLDAFV- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RRVEV------VQPALFAVQTSLAALWRSFGVTPDAVVG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 -FIGGVGAQY--GDTGRWIFAAGAFAASLIW----FPLVGFG---AAALSRPLSSPKVWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Monadio, S
APPLICANT: Monadio, J
APPLICANT: Monadion, J
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Brythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 82.5; 28.0%; Pred. No. 5.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07642734C
Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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LENGTH: 3491 amino ac
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MEDIUM TYPE: Floppy
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Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 60064-3500
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215 SINLLL 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 WDDDVV 205
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                                                                                                                        229 AIKLML
                                                                                                                                                                                                                                       RESULT 4
US-07-642-734C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID, AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                TITLE OF INVENTION: DNA CODING FOR PROTEIN WHICH CONFERS ON BACTERIUM
TITLE OF INVENTION: ESCHERICHIA COLI RESISTANCE TO LO-HOMOSERINE AND METHOD
TITLE OF INVENTION: FOR PRODUCING L-AMINO ACIDS
FILE REFERENCE: 0010-1039-0
CURRENT APPLICATION NUMBER: US/09/396,357
CURRENT FILING DATE: 1999-09-15
EARLER APPLICATION NUMBER: RU98118425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GTLGVDLLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 PLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LEWWFAYLLTSIILTLSPGSGAINTMTTSL-NHGYPAGGVYCWASDRTGDSYCAGWRGVG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 KVEA-----PQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 PKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTLVVDIIVWIGYATLAQRIALMIK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 205;
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19.5%; Pred. No. 0.049;
tive 42; Mismatches 103; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; DB 4; I
0.015;
ches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LLSNAAPIVLDIMRWGGIAYLLWFAVMAAKDA---
VLADIMIR VENYAMIOVICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4608, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                  EARLIER FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.5%;
Best Local Similarity 20.6%;
Matches 36; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match '7.2%
Best Local Similarity 19.5%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Escherichia coli
US-09-396-357-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4608
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                                                                                                                                                                                                                                                                                                                                   205
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                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.7%; Score 80; DB 4, Best Local Similarity 25.2%; Pred. No. 0.46; Matches 52; Conservative 31; Mismatches
                  B: Dehlinger & Associates
350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UTN-97
ATTORNEY/AGENT INFORMATION:
NAME: Perithory, Joanne R.
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: 2000-045
TELECOMMUNICATION INFORMATION:
TELEFAK: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 SR-PLSSPKVWRWINVVVAVVMTALA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNIA...
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
TYPE: IBM Compatible
TYPE: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
CORRESPONDENCE ADDRESS:
                          STREET: 350 TITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-001C-4637
                                                     CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-105-390-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AAPIVLDI----MRWGGIAYLLW-----FAVMAAKDAMTNKVE-----APQIIEETEPT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 VPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPMLMAI----VLTWLNPNAYLDAFV- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 -FIGGVGAQY--GDTGRWIFAAGAFAASLIW----FPLVGFG---AAALSRPLSSPKVWR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 SAPVVFVFPGQGAQWAGMAGELLGESRVFA--AAMDACARAFEPVTDWTLAQVLDSPEQS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.9%; Score 82.5; DB 3; Length 3491; Best Local Similarity 28.0%; Pred. No. 5.8; Matches 52; Conservative 18; Mismatches 53; Indels 63
                                                               Parent No. 6064787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          STREET: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
10S-09-10S-390-64
1S-09-10S-390-64
1 Sequence 64, Application US/09105390
1 PATENT NO. 6288303
2 GENERAL INFORMATION:
2 APPLICANT: Rodriguez, Raymond
2 TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
3 TITLE OF INVENTION: and Genes
4 NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A-
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.DI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
                                               Sequence 2, Application US/08439009A Patent No. 6004787
                                                                                                                                                                                                                                                                                                                                                        ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 3491 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-439-009A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 WDDDVV 205
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        RESULT 5
US-08-439-009A-2
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                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Sequence 4637, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                      88 MAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWVKPML 147
                                                                                                                                                                                                                                                                                 148 MAIVLIWINPN--AYLDAFVFIGGVGAQYGDTGRWIFA-AGAFAASLIWFPLVGFGAAAL 204
                                                                                                                                                                                                                                                                                                                                    37 GLIAVLLVCLISDVFLFI--AGTLGV-----DLLSNAAPIVLDIMRWGGIAYLLWFAV 87
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SEQUENCE CHARACTERISTICS
                         LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G.
                                                                                                                                                                                                                                                                                                                                                                                      54 VPIVPDYIAHMRGGS---
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                                                                                                                US-08-793-044-3
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                                                                                                                                                                                                                                                                                                                                                                                      162 SLSESFGSSPRDGSERKMGAFLIFTEFQGNLITSAMFLTAMAGNPIAQSLAEKTAHVQİT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LGGSAVATDTRN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 RVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFV----FIGGVGAQ---YGDIGRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 112; Gaps
                                                                                                                                                                                                                                                                                            102 isrgfvktglgrrialofvklfgkktlglayslvgvdlilapatpsntaraggimfplik 161
                                                                                                                                                                                                                                                                                                                                           72 DIMRWGG-----IA 80
                                                                                                                                                                                                                                                  29 IKQGIKREGL---IAVLLVCLISDVFLFIAGTL-GVDLL-----SNAA-----PIVL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 IFAAGAFAASLIWFPLVGFGAAALSRPLSSPKVWRWINVVVAVWTALAIKLMLM 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 -----NTLVWFSVLVLMAEQLNKLGFIP----WLSKLIAQGLNGFSWPIVLV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bejainh, Stephane
APPLICANT: Berard, Sylvie
APPLICANT: Gervini, Riccardo
APPLICANT: Mallet, Jacques
APPLICANT: Mallet, Jacques
TITLE OF INVENTION: NOVEL VESICULAR ACETYLCHOLINE CARRIER
NUMBER OF SEQUENCES: 12
                                                                                                                                                           Query Match 6.6%; Score 79; DB 4; Length 478; Best Local Similarity .19.7%; Pred. No. 0.84; Matches 58; Conservative 45; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                  81 YLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01073
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REPERENCE/DOCKET VINDER: ST94066-US
TELECOMMUNICATION:
TELEPHONE: (610) 454-3816
                                                                                         ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR 94/10044
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TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4637
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: P. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-793-044-3
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                                                                                                                                                                                                                                                                                                                                             67 APIVLDI----MRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEET-EPTVPDDTPLGGSAV 122
                                                                                                      9 TGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVC--LISDVFLFIAGTLGVDLLSNA 66
                                                                                                                                                                                                                                                            -----EGPTLVSEVWEPTLPPPTLANASAY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
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  DB 4; Length 530;
                                                   74; Indels
                                                                                                                                   167 --IGGVGAQYGDTGRWIFA---AGAFAASLIWFPLVGFGAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 PLLIGLGVMFASTVMFAFAEDYATLFAAR----SLOGLGSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
Query Match 6.6%; Score 79; DB Best Local Similarity 23.5%; Pred. No. 0.98 Matches 52; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82:
TELECOMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: THOMAS G. PLANT
STREET: LILLY CORPORATE CEN
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4545 amino acids
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2276 ELVERLTALGSEVAVEACDVADRDALAALLAGLPEERPLVAVLHAAGVLDDGVLDSLTSD 2335
                                                                                                                                                    2336 RVDA-VLRDK------VTAARHLDELTADLPLDAFVLFSSIVGVWGNGGQAVYAAANAA 2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IMBIFITGLLLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
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                                                                                                                         129 RVRVEVSVDKQRVWVKPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Resteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 79; DB;
21.5%; Pred. No. 22;
:ive 35; Mismatches
                                                                                                                                                                                                                                      2388 LDALAQRRRARGARAASIAWGPWAGAGMAS 2417
                                                                                                                                                                                                           185 -----GAFAASLIWFPLVGFGAAA 203
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STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08804198 Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Conservative
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LENGTH: 4550 amino act
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MOLECULE TYPE: peptide
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ADDRESSEE: PAUL R. C
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46285
                                       102 QIIEE---
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                                     2331 RVDA-VLRDK------VTAARHLDELTADLPLDAFVLFSSIVGVWGNGGQAVYAAANAA 2382
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3 IMELPITGLILGASLILSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFIAGTLGVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 LSNAAPIVLDIMRW------GGIAYLLWFAVMAAKDAMTNKVE------AP 101
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                                                                                                 ---GGIAYLLWFAVMAAKDAMTNKVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DeHOff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.6%; Score 79; DB 2
Best Local Similarity 21.5%; Pred. No. 22;
Matches 58; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             2383 LDALAQRRRARGARAASIAWGPWAGAGWAS 2412
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COMPUTER READABLE FORM:
MEDIUM TYPE: FOOPPY disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08804227C
Patent No. 5876991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                               LSNAAPIVLDIMRW-----
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ADDRESSEE: THOMAS G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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US-08-804-227C-8
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Cloning, Tissue Distribution, and Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 -----VŠLGGTLVGVIPAFLLSLVTRFTKHVRI---IEPGFVFVISYLSYLTSEMLSLSA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AGTLGVDLLSNAAPIVL----DIMRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IFITGL------LLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finnegan, Henderson, Farabow, Garrett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 78.5; D
Best Local Similarity 20.4%; Pred. No. 2.1;
Matches 53; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 --VFGESLLNDAVTVVLYNVFESFVTLGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/677,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          Sequence 11, Application US/09097053
Patent No. 6392025
                                                                                                                                                                                                                                                                 APPLICANT: Brant, Steven R. APPLICANT: Wun, Chris C.H. APPLICANT: Donowitz, Mark APPLICANT: Tee, Chung-Ming TITLE OF INVENTION: Functional TITLE OF INVENTION: Punctional TITLE OF INVENTION: NUBBS. 12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESSE: Rinnegan, Hender
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                    358 PVIWTWNTAFVLLTLVFISV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopre
COMPUTER: TEA
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APPLICANT: Brant.
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                                                                                                                                             RESULT 13
US-09-097-053-11
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Punctional Analysis Of The Human Na+/H+ Exchanger Isoform,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
2336 RVDA-VLRDK------VTAARHLDELTADLPLDAFVLFSSIVGVWGNGGQAVYAAANAA 2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * 160 YLDAFVFIG------GVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSS 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ATDTRNRVRVEVSVDKQRVWVKPMLMAIVLTWLNPNA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 IFITGL------LLGASLLLSIGPQNVLVIKQGIKREGLIAVLLVCLISDVFLFI
                                                                                                                                                                                                                                                                                                          APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tee, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Punctional Analysis Of The Human Na+
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunner
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COMPRIX: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
6.6%; Score 78.5; Di
Best Local Similarity 20.4%; Pred. No. 2.1;
Matches 53; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/677,734A*
FILING DATE: 10-UUL-1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFRENCE/DOCKET NUMBER: 05387.0043-00;
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                     2388 LDALAQRRRARGARAASIAWGPWAGAGMAS 2417
                                                                    -----GAFAASLIWFPLVGFGAAA 203
                                                                                                                                                                                                                                        Sequence 11, Application US/08677734A Patent No. 5871919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 831 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 TVPDDTPLGGSAV-
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Cloning, Tissue Distribution, and Punctional Analysis Of The Human Na+/H+ Exchanger Isoform,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 ------LGGTLVGVVFAFLLSLVTRFTKHVRI---IEPGFVFIISYLSYLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IAYLLWFAVMAAKDAMTNKVEAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 LTWINPNAYLDAFVFIG------GVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 IFITGL------LLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLISDVFLFI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%; Score 76.5; DB 2; Length 834; 18.7%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 --VFGESLINDAVTVVLYNVFESFVALGGDNVTGVDCVKGIVSFFVVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677.734A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches
          203 ALSRPLSSPKVWRWINVVVAVVMTALAI 230
                                                            360 -----NPFIWTWNTAFULLTLVFISV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-JUL-1996
CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               Sequence 10, Application US/08677734A Patent No. 5871919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AGTLGVDLLSNAAPIVL-----DIMRWGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brant, Steven R. APPLICANT: Yun, Chris C.H. APPLICANT: Donowitz, Mark APPLICANT: Tse, Chung-Ming TITLE OF INVENTION: Cloning, TITLE OF INVENTION: Function TITLE OF INVENTION: NHB3. NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 05
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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Matches 50; Conserva
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                                                                                                                                                                                  RESULT 15
US-08-677-734A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Yun, Chris C.H.
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Punctional Analysis Of The Human Na+/H+ Exchanger Isoform,
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
306 IL-AITFCGICCQKYVKANISEQSATTVRYTMKMLASGAETIIFMFLGISAV-----D 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 QIIBETEPTVPDDTPLGGSAV-----ATDTRNRVRVEVSVDKQRVWVKPMLMAIV 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 LIWINPNAYLDAFVFIG-----GVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 SEMLSLSAIL-AITFCGICCQKYVKANISEQSATTVRYTMKMLASSAETIIFWFLGISAV 359
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION UNUBER: US.08/677,734A
FLING DATE: 10-JUL-1996
FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
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CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 18.7%; Pred. No. 3.7;
Matches 50; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08677734A Patent No. 5871919
                                                                211 PKVWRWINVVVAVVMTALAI 230
                                                                                                              358 PVIWTWNTAFVLLTLVFISV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9: SEGURENCE CHARACTERISTICS:
LENGTH: 834 amino acids
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STRANDEDNESS: si
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Search completed: April 24, 2003, 18:24:13 Job time : 21 secs

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RESULT 1
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LOCUS
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                                                                       April 26, 2003, 18:49:18 ; Search time 6117.94 Seconds (without alignments) 11293.030 Million cell updates/sec
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2374
1 agatactoctttggaagaaa......gtaacaccttcagcaaatgg 2374
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                    2054640 seqs, 14551402878 residues
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 st
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Maximum DB seq length: 200000000
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AE000382 ESCHELL.
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AC020884 Mus muscu Sequence Mesorhizo I86263 Sequence 17 AE007056 Mycobacte Z74025 Mycobacteri Corynebac Agrobacte AB011413 Streptomy AP002563 Escherich C.glutamicu Corynebac Agrobacte AJ311775 Rhodococc AE005530 Escherich M37389 Pseudomonas Sequence Sequence AL357613 Streptomy AL591788 Sinorhizo U34849 Mycobacteri Streptomy Xanthomor Sequence Streptomy AX127147 Sequence AX063767 Sequence Sequence Salmonel Sequence Sequence Sequence Seguence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence AL049863 AE011965 AX347518 AX347541 AX347564 AX431662 AX244059 AB083133 AE008076 AL450223 AX343066 ALIGNMENTS SUMMARIES RFA311775 SC5H1 AE011965 SC5F8 SME591788 MBU34849 186263 AE007056 AE005530 AB011413 AP002563 AX244059 AB083133 AX123539 AX123538 AX067087 AP003001 AC020884 AP005277 AX127147 AE008076 CGLYSEG SEIGRA B 110000 22929 256050 Length 345783 15586 33285 306250 Query Match 100.0 100.8 100.8 100.8 798.8 708 627 112.4 112.2 111.2 109.8 105.2 140.6 135.6 122.8 121.2 116.4 100.8 100.8 485.2 159.4 90 Result ģ

CGLYSEG/c
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ACCESSION
C.glutamicum lysE and lysG genes.
ACCESSION
X96471.
VERSION
X96471.1 GI:1729753
KEYWORDS
SOURCE
COTYNebacterium glutamicum.
ORGANISM
COTYNebacterium glutamicum.
ORGANISM
COTYNebacterium glutamicum.
COTYNebacterium glutamicum.
COTYNebacterium glutamicum.
Actinomycetales; Corynebacteria; Actinobacteriaceae;
Actinomycetales; Corynebacteriumes.
COTYNebacterium.
RACTHORS
ACTINOMYCETALES
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Pred. No. is the number of results predicted by chance to have a

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RVLVSRTQPAKATEAGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTW
PPPVFNEVASWGGATUTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPS
AEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDBIPIDTPMYWQRWRLESRSLARL
TDAVVDAAIEGLRP"
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SUPPLEIGAGTGVDLLSNABPFULDIRKWGGIAYLLWPRVMARCDAWTRKVEAPQIIE
ETEPTVPDDTPLGGSAVATDTRNRVRYEVSVDKQRVWYKPMLAAIVLTWLNPRAYLDA
FVFIGGVGAQYGDTGRWIFAACAFAASLIWFPLVGFGAAALSRPLSSPKVWRNINVV
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, Postfach 1913, D-52425 Juelich, FRG
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A new type of transporter with a new type of cellular function:
L-lyabine export from Corynebacterium glutamicum
Mol. Microbiol. 22 (5), 815-826 (1996)
97126810
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Direct Submission
Submitted (07-MAR-1996) M.M. Vrijic, In
Submitted (07-MAR-1996) M.M. Vrijic, In
1, Forschungszentrum Juelich, Postfach
Location/Qualifiers
1. .2374
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1 (bases 1 to 2374)

1 (bases 1 to 2374)

Vrlijc, m. and Eggeling,L.

PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY BOOSTED

ACTIVITY OF EXPORT CARRIERS

Patent: WO 9723597-A 2 03-JUL-1997;

KERNFORSCHUNGSANLAGE JUELICH (DE); VRLIJC MARINA (DE)
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                    94 ATTGCGGCCTTAGTTACTTCTGAAAAGGTTCAGGGTTTTTCACTTCTTCGCCCGCAGGAA
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Corynebacterium glutamicum
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomyceteles, Corynebacterineae, Corynebacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2374;
                                                                                                                                                                                    linear
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                                                                                                                                                                                    DNA
                                                               lery Match 100.0%; Score 2374; st Local Similarity 100.0%; Pred. No. 0; tches 2374; Conservative 0; Mismatches
                                                                                                                                                                                A93933 2374 bp
Sequence 2 from Patent W09723597,
A93933
A93933.1 GI:6742037
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SION
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CAACAACTIG	CGGCATCAAC CGGCATCAAC	CATCAGTTTG CATCAGTTTG	CACCTTGGGG	CCAGATCAGG	TTGCGCGCCG TTGCGCGCCG	GGTCAGCACG GGTCAGCACG	8=8	ATCGGGCACG ATCGGGCACG	GCGTCTTTC 	AATATCGAGC AATATCGAGC	gaacaaaaag gaacaaaaag	AATTCCTTGT AATTCCTTGT	CAAAAGCAGA CAAAAGCAGA	agtaaaatga agtaaaatga	CACTTTGCTC	TTCCCCCTCG	GGTATCGCGC
541	y 601 5 1774	y 661 0 1714	y 721 o 1654	y 781 5 1594	y 841 b 1534	y 901 b 1474	y 961 b 1414	y 1021 b 1354	1081	y 1141 b 1234	y 1201 b 1174	y 1261 b 1114	y 1321 b 1054	у 1381 b 994	14.	y 1501 b 874	1561
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_	TGGGCCAGGCAGAGTAACACTTCAGCAAATGG 2374	COY 2341 TO TO TO TO TO TO TO TO TO TO TO TO TO	OY OY OY OY OY OY OY OY OY OY OY OY OY O	
	237	2341	· & 8	
	ATTGCGGCCTTAGTTACTTCTGAAAAGGTTCAGGGTTTTTCACTTCTTCGCCCGCAGGAA 2340	2281	& ^점 .	
•	CCTGGAATCTAGATCTAGCTAGACTCACAGACGCCGTCGTTGATGCAGCAATCGAGGG 2280 	2221	රි සි	
	AGAAGTGATCCTCCTCGATGAGATACCCATTGACACACCGATGTATTGGCAACGATGGCG 2220	2161	ଧ ସ	
	CCGAGGCCTTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCTCCCATGCTAAAAGCAGG 2160 	2101	රු පු	
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	CTCATTGCGGGGATGCCTACATGGTTGATGGGGAAACTAGATTGGGCTGCGGATGCCCGTCTT 1980 	1921	8 8	
	CGTGGCGGGATGTGAAGTAGAACTTGGAACCATGCGCCACTTGGCATTGCAACCC 1920 	1861	8 8	
	CACATTATCCTTGCTGCGGGGGGGGGGGGGTTTTAGGGGGGGG	1801	୍ଧ ୍ଧ	
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	AATCCCGTTAACCATCGCCATCAACGCAGATTCGCTATCCACGTGGTTTCCTCCCGTGTT 1740	1681	පි ර	
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COMMENT FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPSNRTDVCVLDLQLGGIDGIDTATRLMETTPDLAVLIVTSHARPRQLKRALAAGVLG
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                                               WHGTCTYPRAIKDVLADVDLLHRENVKVGALSGGEQRRLDLACALLGDPSILFLDEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVREATTNILRHSDATDATLTLSSTEVRMDNNGVNKDIGRLSGLSALRSRAESAGMTL.
IVSREDDQFSVRMLINAPANTPABKEA"
6139. .6750
              KTSTLEVIEGLSAPSSGTVRISGLDPVADRAILRPELGIMLQSGGLPSQLTVAETMDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Two-component system, sensory transduction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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//gene="cg10946"
3063. .3883
//gene="Cg10946"
//note="PP00005:ABC transporter
TIGR00960:3a0501802: Type II (General) Secretory Pathway
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitasato University.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGROI188:drrA: daunorubicin resistance ABC transporter
ATP-binding subunit
TIGR01189:ccmA: heme exporter protein CcmA"
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TIGR01187:potA: spermidine/putrescine ABC transporter
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TIGR01166:cbiO: cobalt transport protein ATP-binding
                                                                                                                                                                    1.333150

| Organism="Corynebacterium glutamicum ATCC 13032"
|strain="ATCC 13032"
| Ab xref="taxon:196627"
|note="ATCC 13032"
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                                                                                                                                                                                                                                                                                                                         gene
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STERRAKQLOGGNFYFTLFRAFSTEKVAKWKORQCRIMDQAAAIREESN"
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AVKTPEKASQASARAAVDTAVASGKVAGIGELSI AVNILAAVLLLAGMRVTTGELGPGÖ
TLAI VGVAVYLSEPIRLLSNSI INASAT HAGABERKANFLILLDESQAQYESSETINDGE
FLVI VPPASTILPHQADI FEGTILRSNI SMMHEDNVPI DDPQVIRASGLTDI
I EVDGLDAPVRDTGSNI SGGQRQRVALARALHADAEVI VIMDPTSAVDSVTEVSI AQG
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/transl_table=11
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system, ATPase component"
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/db_xrefE="GI:2132719"
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HALKNLDPRNLVPGEVMSRSTADADSSTRIFGQIGTGVSAATGFLGSATYLLISDWLV
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FEATURES Location/Qualifiers source 1.349980 /organism="Corynebact /bb_xref="teaxon:1718" /note="569" Location/Qualifiers 1.000.001 1.549.980" BASE COUNT 80727 a 91049 c 97618 g 8	Query Match Best Local Similarity 100.0%; Score 2 Matches 2374; Conservative 0; Misma Qy 1 AGATACTCCTTTGGAAGAAACCATGTAGGAT Db 127595 AGATACTCCTTTGGAAGAAACCATGTACGAT	Oy 61 TCTTACGTGGGTATTTCTTCCTACGGTCCAG Db 127655 TCTTTACGTGGGTATTTCTTCCTACGGTCCAG Oy, 121 GGCGGAGGAGGGCTGCCCGCTTCTGATTCATC Db 127715 GGCGAGGAGGCTGCCCGCTTCTGATTCATC OY 181 GGTGGAGGAGGCTGCCGCTTCTGATTCATC OY 181 GGTGGAGGAGGATGCTGCCGCTTCTGATTCATC OY 181 GGTGGAGGAGGATGCTGCTGATCATCATCATCATCATCATCATCATCATCATCATCATCA	Db 127775 dergehechackedekehrenkergahaktr Qy 241 TGGCGTCATTGCTTTCTCACCACTGCGCAGG	361 127955 421 128015	Oy 481 GACCACTGCATTGATTGGTGCTTCGTCAGTTG Db 128075 GACCAGTGCATTGATTGGTGCTTCGTCAGTTG Oy 541 CAACAACTTGGAGTTTTCTGACGCGGGTTGG Db 128135 CAACAACTTGGAGTTTTCTGACGCCGAGTTGG Oy 601 CGGCATCAACATTGGGGGAAGGCCACCGATTG	128195 661 661	128 128 128
	1741 CAACGAGGTAGCTTCTTG 1741 CAACGAGGTAGCTTCTTG 329385 CAACGAGGTAGCTTCTTG 1801 CACATTATCCTTGCTGCG 329445 CACATTATCCTTGCTGCG				Oy 2281 ATTGCGCCTTAGTTACTTCTGAAAGGTTCAGGGTTTTTCACTTCTTCGCCCGCAGGAA 2340	RESULT 4 AX121147 LOCUS 34220 bp DNA linear PAT 11-MAY-2001 DEFINITION Sequence 7063 from Patent EP1108790. ACCESSION AX127147 AX114121 VERSION AX127147 AX114135 KEYWORDS	SOURCE Corynebacterium glutamicum. ORGANISM Corynebacterium glutamicum ORGANISM Corynebacterium Bacteria; Firmicutes; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium. Corynebacterium. Corynebacterium. Tobases I to 349980) AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 7063 20-JUN-2001;

SGCCTGCTCACGGACAAATATCTCGATGG 300 GAGCAGCTGGACAACAGCCTTGATTCACT 540 THGTTGCAGTCAGCTGCCAACAATGGTCT 240 KGAGGCGATCGATGAGATTTCCCACGACGC 600 TCCAAAACCGGGAAAACTAACCGATCAA 660 GCGTCCAAATACGCATTCGGGTTCAACCA 900 ACTGCCACGACGACGTTGATCCAGCGCCA 720 g (3.309.400) split in 11, seg 7063 480 CAGCCAAGCTATTCCATCATTAATCGTTG 180 PAGTCCCTGTCTGAGGGCATGTTGAACGT 360 GACATCGCCCAGGAACGCGGGCAGTCACT 420 GAGCTCACAGCGGAGGCGGCTGAGTTCAT 120 GCTGCTGCGCCGAAACCCACCAGCGGAA 780 GCGAAAATCCACCGTCCGGTGTCGCCGTA 840 0; Gaps TTGCGTGACATTGTTGCGTCTGGAAAGGC 60 GAGCAAGGAGAGTACGGCGCGGATACCGT DB 6; Length 349980; 0; Indels terium glutamicum" 2374; D No. 0; matches 80586 t (AB)

QY 901 GGTCAGCACGATTGCCATCAACATGGGCTTTACCCAAACCCGCTGCTTATCGACGCTCAC 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Oy 961 CTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGAACCGCCCAAAGGCGTGTC 1020 Db 128555 CTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCCACCGCCGAACCGCCCAAAGGCGTGTC 128614
OY 1021 ATCGGGCACGGTTGGTTCTTCTTCAATGATCTGTGGGGGCTTCCACCTTGTTTGT
OY 1081 GGCGTCTTTCGCTGCCATGACGGCAAACCATAACAGGTAAGCGATGCCACCCCAGCGCAT 1140
OY 1141 ANTATCGAGCACGGCGCGGCATTGCACAAAGATCAACGCCCAAGGTGCCGGCGAT 1200 Db 128735 AATATCGAGCACGATGGGCATTGGACAAAGATCAACGCCCAAGGTGCCGGCGAT 128794
OY 1201 GAACAAAAAGACGTCAGAAATTAAACACACGAGAAGAACGCCAATGAGTCCTTCGCGCTT 1260 Db 128795 GAACAAAAAGACGTCAGAAATTAAACACACGAGAAGAACGCCAATGAGTCCTTCGCGCTT 128854
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OY 1321 CAAAAGCAGCCTGTAATGAAGATTTCCATGATCACCATGGGACTATGGAAGTACTTA 1380
OY 1381 AGTAAAATGATTGGTTCTTAACATGGTTTAATATAGGCTTCATGAACCCCATTCAACTGGA 1440 DD 128975 AGTAAAATGATTGGTTCTTAACATGGTTTAATATAGCTTCATGAACCCCATTCAACTGGA 129934
QY 1441 CACTITIGETCTCARTGATGAAGGGAGCTTCGAAGGCGCCTCCTTAGCCCTTTCCAT 1500 D 129035 CACTITIGETCATCATGAAGGCAGCTTCGAAGGCCCTCCTTAGCCCTTTCCAT 129094
OY 1501 TICCCCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGTCGAGTGTT 1560 Db 129095 TICCCCCTCGGCGGTGAGTCAGCGGTTAAAGCTCTCGAGCATCACGTGGGTCGAGTT 129154
OY 1561 GGTATCGCGCACCCAACCGGCCCAAGCGACCGAAGCGGGTGAAGTCCTTGTGCAAGCGGC 1620
OY 1621 GCGGAAAATGGTGTTGCTGCAAGCAGAACTAAAGCGCAACTATCTGGACGCTTGCTGA 1680 DD 129215 GCGGAAAATGGTTGCTGCAAGCAGAAACTAAAGCGCAACTATCTGGACGCCTTGCTGA 129274
OY 1681 AATCCGTTAACCATCGCCATCAACGCACATTCGCTATCCACATGGTTTCCTCCCGTGTT 1740
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OY 1921 CTCATTGCGGGATGCCTACATGGTTGATGGGAAACTAGATTGGGCTGCGATGCCCGTCTT 1980

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PEPVTNEVSASGGATLTLRLEDEAHTLSLLERGDVLGAVTREANPVAGCEVVELGTMR
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TDAVVDAAIEGLRP
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Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria: Firmicutes; Actinobacteria; Actinobacteriaceae;
Actinomycetales; Corynebacterineae; Corynebacterium:
I (Dases I to 93)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. corynebacterium glutamicum genes encoding metabolic pathway
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                                            129634
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1321 CAAAAGCAGACCTGTAATGAAGATTTCCATGATCACCATCGTGACCTATGGAAGTACTTA 1380
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                                                                                                                                   Db 129635 TGTGGGGGCGCGGGGGGTATCCATTGTCCCGTCGGCGGAAGGTTTTGGTGAGGCAATTCG
                                                                                                                                                                                                                              Db 129695 CCGAGGCCTTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCTCCCATGCTAAAAGCAGG
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                             2041 TGTGGGGCGCAGGCGCGTATCCCATTGTCCCGCGCAAGGTTTTGGTGAGGCAATTCG
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BASF AKTIENCESELLSCHAFT (DE)
Location/Qualifiers
1. 993
/organism="Corynebacterium glutamicum"/db xref="taxon:1718"
101. 973
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GRANATGATTGGTTCTTAACATGGTTTAATATATAGTGTTCATGGAACCCCATTGGTTCAATGATTGGTTCTTAACATGGTTTTAATATATAT	1411 CACTTTGCTCTCAAATCATTGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCCCTTTCCAT	1801 CACATTATCCTTGCTGCGGCGTGAGATGTTTTAGGAGCGGTAACCCGTGAAGCTAATCC		

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terium glutamicum genes encoding metabolic pathway
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terium glutamicum.
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; Rirmicutes, Actinobacteria, Actinobacteridae,
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/db_xref="taxon:1718"
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ENGESELLSCHAFT (DE)
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541 CGTGGCGGGATGTGAAGTAGTAGTAGAACTTGGAACCATGCGCCACTTGCCATTGCAACCCC 600
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1 (bases 1 to 870)

Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Vokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Novel polymucleotides
Patent: EP 1108790-A 3456 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)

Location/Qualifiers
                                                                                             ACCCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGCGCGCGTCGATGGTCC
                                                                                                                                                          TGTGGGGCGCAGGCGCGTATCCATTGTCCCGTCGGCGGAAGGTTTTGGTGAGGCAATTCG
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Actinomycetales, Corynebacterineae, Corynebacteriaceae,
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/organism="Corynebacterium glutamicum"
/db_xref="taxom:1718"
_236 c 245 g 197 t
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Best Local Similarity 100.0%; Pred. No. 4.4e-203;
Matches 870; Conservative 0; Mismatches 0;
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Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria;
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Seguence 3456 from Patent EP1108790.
AX123540
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PAT 24-JAN-2001
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Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. corynebacterium glutamicum genes encoding metabolic pathway
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CTATCTGGACGCCTTGCTGAAATCCCGTTAACCATCGCCATCAACGCAGATTCGCTATCC
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                                                                               CTATCTGGACGCCTTGCTGAAATCCCGTTAACCATCGCCATCAACGCAGATTCGCTATCC
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Actinomycetales, Corynebacterineae, Corynebacteriaceae,
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/organism="Corynebacterium glutamicum"
/db xref="taxon:1718"
101. .802
/note="RXA01394"
/codon_start=1
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BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
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Sequence 53 from Patent WO0100843.
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AX063771.1 GI:12541483
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      /protein_id="CAC25127.1"
/boxein_id="CAC25127.1"
/boxein_id="C112541484"
/translation="MENFITGLILGASLILSIGPONVLVIKGGIKREGLIAVILVCLI
SDVFLF1AGTILGVDLISNAAPIYLDINKWGGIAYLLWFAVMAAKDAMTNKVBAPDITE
SEPFYVBDDFFLGGSAVATDTRNRVRVENSYDKGRVWYKPMLMAIVJWINPNAYLDA
FVFITGGYGQYGDTGFWIFAAGAPAASLIWFPLVGFGAAALSRPLSSFKVWRNINVVV
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                                                                                                                 Query Match 34.6%; Score 822; DB 6; Le Best Local Similarity 100.0%; Pred. No. 2.9e-191; Matches 822; Conservative 0; Mismatches 0;
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RESULT

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RVVWTPLAIKLIALMGA
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                                                                                                                                                                                           Corynebacterium.

1 (bases 1 to 822)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O., Haberhauez Kim, J.W., Lee, H.S. and Hwang, B.J.
Corynebacterium glutamicum genes encoding metabolic pathway
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Corynebacterium glutamicum
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
Actinomycetales, Corynebacterineae; Corynebacteriaceae;
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100.0%; Pred. No. 2.9e-191;
ive 0; Mismatches 0;
           DNA
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BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
Sequence 51 from Patent WOO166573.
AX244059
AX244059.1 GI:15859122
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Published only in Database (2002)
2 (bases 1 to 1771)
Itaya, H., Kimura, B., Kawahara, Y. and Sugimoto, S.

Direct Submission
Submitted (04-APR-2002) Hirosh Itaya, AJINOMOTO CO., INC,
Permentation & Biotechnology Laboratories; 1-1, Suzuki-Cho,
Rawasaki, Ku, Kawasaki, Kanagawa 210-8681, Japan
(B-mail:hiroshi itaya@ajinomoto.com, Tel:81-44-244-7123(ex.4146),
Pax:81-44-222-0129)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium efficiens DNA.
Corynebacterium efficiens
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinea; Corynebacterium.
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                                                           Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. Novel polynucleotides
Patent: EP 1108790-A 3455 20-JUN-2001;

KXOWA HAKKO KOGYO CO., LTD. (JP)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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1 (Dases 1 to 627)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynucleotides
Patent: EP 1108790-A 3454 20-JUN-2001;
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                                                                                                 TITLE
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VTHPDLANNYGPPAGSAETNPGRILREDLKSHRDELLISSKAGWDMWPGPYGFGGSRK
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WVLREQREYGAGLP
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                                                                                                                                                           and Haberhauer, G.
                                                                                                                                                   Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer corynebacterium glutamicum genes encoding proteins involved in membrane synthesis and membrane transport Patent: WO 0100805-A 669 04-JAN-2001; BASF AKTIENGESELLSCHAFT (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 GGGGGAGGAGGCTGCCGCTTCTGATTCATCAGCCAAGCTATTCCATCATTAATCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            850 GAACAATATTGATATGGTCCGCAAGCTCAATGACATCGCCCCAGGAACGCGGGCAGTCACT
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7
                                                Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
Actinomycetales, Corynebacterineae, Corynebacteriaceae;
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    1. 993
    /organism="Corynebacterium glutamicum"

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Pred. No. 2.3e-108;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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Corynebacterium glutamicum
Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                            101. .973
/note="RXN03164"
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                                                                                                                             (bases 1 to 993)
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Matches 499; Conservative
                                                                                                     Corynebacterium
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REFERENCE AUTHORS

AUTHORS TITLE JOURNAL MEDLINE REFERENCE

JOURNAL

TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVTHIGYNRERDI IAKI PGYDVVVGGHSHTLLSNTDPRAAGPYFTMVDNPGGYKVPVV
QAASYSKYLGEFKVVPDDNGVVKSASGDPI FLDKS I TPDPAVLARI KELGAPI EALKN
KEVAETTDY UIGSRENCFRAKCEMGNIVSDA LIDRYKGQGVE IVI SNGGELRASI DKG
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GTVEEEFLNOMKPDAVTLGNHEFDDGESALVPYLDKAKFPIVSANVMPNDKSGAAGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPMWRYLRBFLSDPRVIELNKAIWYPILYGLVLTTRPKKSGANYARIWNOERNESPLR
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(codon start=1
(rans]_table=11
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protein id="BAB50005.1"
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                                                                                                                                                                                                                                                                                                    |431. .3931
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(gene="mlr3017"
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/gene="mlr3019"
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CRRLVVAAPSYLAREGEPIAPDELSRHEAILFVRAGTSIRWTFRRGAEEVSLAGGGRL
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                                      BCT 15-MAY-2001
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DDIAPTVAFLASDEAAWLTGERINASGGAR"
                                                                                                                                                                                                                                                                                      I (sites)
Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto,S., Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T., Kibhida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A., Mochizuki,Y., Nakayama,C., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.
Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti
DNA Res. 7 (6), 331-338 (2000)
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Direct Submission
L Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research, Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:Kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp/
Tel:81-438-22-3935 (ex. 2338), Fax:81-438-52-3934)

F On May 11, 2001 this sequence version replaced gi:11994976.
                                                                                                                                                                                                   Mesorhizobium loti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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/product="short chain dehydrogenase or 3-ketoacyl-CoA
                       AP003001 345783 bp DNA linear BC
Mesorhizobium loti DNA, complete genome, section 8/21.
AP003001 BA000012
AP003001.2 GI:14023393
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product="transcription regulator"
protein_id="BABS0000.1"
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/product="homospermidine_synthase"
                                                                                                                                                                           Mesorhizobium loti (strain:MAFF303099) DNA
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/strain="MAFF303099"
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/db_xref="GI:14023395"
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/gene="mll3011"
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994. .1740
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gene="mlr3014"
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transl_table=
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/transl table=
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AP003001/c
                                                     DEFINITION
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GGCATCAACATTTGGGCGAAGGCCACCGATTCCAAAACCC
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Hinkle, G., Slater, S.C. and Goodner, B.
Direct Submission
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8472 bp
Agrobacterium tummefaciens str. C58
of 254 of the complete sequence.
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/strain="C58"
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AE008076.1 GI:15156608
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JOURNAL
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                     249802
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AKDDAIIAISWSGESKEMLGIVAYSRRFSIPLIAVTSGETSALARAADVVLLLPRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACPHGLAPTTSTLLQLVIGDALAIALLEARGFTPDHFRTFHPGGOLGANLTWVSBIMR
VGDQMPLAVLGTKMPEAVMTLSQKKVGCVLIVDANGELAGIITDGDVARNLHRNLADV
IVDEVMTRTPKTVDPQTLAGTAIALLNEHNIGALVVTRNNMPLGVVHFHDLLRIGAA"
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AMMAEALTADGHSVICIDRRGPLKGSTAATTALVQFEIDQPLSTLSYMIGKAKAQQAW
KRRIALSIUNAGRIBDLAIDCRLRRTPSLYLAGTLGPARRREBEARRAGGVAATYL
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                                                                                                                                                                                                                                                                                                                                                                                            RVEITOINPPANLIESMGROMTAERNKRAOILAAEGIKOSOILEAEGRKEAAFRDAEA
RERSAEAEARATOVVSEAISKGDVQALNYFVAOKYTEALGKIGTATNSKIVLMPFEAS
SLIGSLGGIGEIAKEVFRSEGTTGAORQAARPPVVRPSEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MFDRIISELGPWNWWVLGFVLLVMEIIAPGIFMLWIGIAALIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVSLLIWDAAIWTWQVQVLAFLALSLVSAYVGKKLMGGRDQPTDQPLLMRRGAQMVGR
MATLARPIKDGRGRIKLGDTLWRVSGPDLPAGTQVRVTSAADTDLELTVERV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MHARSLDKKPLDROASIDSALRTVATEQAGIAALAEALENGLAA"
                                                                              IWEASDPYLYLRATADGRVICGGEDEDFADETRRDELIADKSARIADKLGRLFPYLDV
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                                                                                                                                                                                                                                                                                                                                                                             AYQVSGLQNAILNLTMTNIRTVMGSMDLDELLSNRDAINERLLRVVDEAAHPWGIKIT
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Pred. No. 1.6e-30;
0; Mismatches 240;
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9912. .10376
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                                                                                                                                                          /gene="mlr3021"
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11830. .13626
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trans table=
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Best Local Similarity 57.3%;
Matches 367; Conservative (
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--GACGCCTGCTCGACGCTCGGAAGGGCTCGGTGTC 249758
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Agrobacterium tumefaciens str. C58 (Cereon).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                     GGCGTCATTGCTTTCTCACCTTGCGCAGGCCTGCTCACGGACAATATCTCGATGGA
                                                                                                                                                    GCTCGATCGTGTTCTCGCCGTGGCCCAGGGCATGCTGACCGACAAATATCTTGGCGGC
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Hinkle, G., Slater, S.C. and Goodner, B.
Complete Genome Sequence of Agrobacterium tumefaciens CS8
(Rhizobium radiobacter C58), the Causative Agent of Crown Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street, Cambridge, MA 02139, USA Location/Qualifiers
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note="(AE005408) putative adhesin"
/codon_start=1
/transl_table=11
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gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6074 CGCAGATGGCAATTGCCTGGGTTCTGCGCGGCGCGCCG------CATTA 6115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITACGIGGGTATITICITICCTACGGTCCAGAGCTCACAGCGGAGGCGGCTGAGTTCATGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGTCATTGCTTTCTCACCACTTGCGCAGGCCTGCTCACGGACAAATATCTCGGAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5669 ACACACCGCTTGAGGAAACCTGCGGCGCTGGACCTGGACGAGATCGTGCGCTTCGGCAAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5894 GCTCCATCGTCTTTCGCCGCTGGCGCAGGCATGCTGACGACGAAATATCTGGGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6176 ATAATGCCGAGTTCTCTACCGAGGAGCTGGCCGAATCGACGTTACGCCAAGGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5789 Addarcroddacecccrocarcarcacaecaecaecaacharrodardarcaacaecaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGTGCATTGATTGGTGCTTCGTCAGTTGAGCAGCTGGACAACAGCCTTGATTCACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cercadearidarindecedaageceneresaacadeareaagacidecederesaaageacide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTCGGAAAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5729 TCTATGTCGGCATCTCCTCCTACAACTCGAAGCGCACCCGCGAGGCCGCCGCTATCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 CGGAGGAGGCTGCCCGCTTCTGATTCATCAGCCAAGCTATTCCATCATTAATCGTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCAGAGGGTTCCCGCGCCAGCCAGGGTAAGTCCCTGTCTGAGGGCATGTTGAACGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6014 GCAATGTCGAAAACATCCGCGCGCTGAACAGCATTGCCGAGCGGCGTGGCCAGACGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 164.4; DB 1; Length 8472; Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.9%; Score 164.4; DB 1;
Best Local Similarity 57.2%; Pred. No. 2.7e-29;
Matches 359; Conservative 0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1740 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGAHGFERTDGVDKPHGPWGSGADIF"
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TTKYLGGVPDGSRASQSKSLNPAFLNERNVENI RALNSI AERRGQTLAQMAIAWVLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHQVKPRFCSBFGFQSYTSMPVIRTYAEDKDMNIASPVIELHQKNVGGNERIAGTMFR
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6465. .6791
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Search completed: April 27, 2003, 00:07:17
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Database

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Medicago truncatula
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7390
Email: gdmay@noble.org
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BQ155035.1 GI:20292094
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BH770958 LLMGtag68
AF075981 AF075981
AL151258 Anopheles
AL108460 Drosophil
                                                                                          (without alignments)
12154.292 Million cell updates/sec
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                                                                           April 26, 2003, 20:02:03 ; Search time 3163.33 Seconds
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          GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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FEATURES

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2051 AGCTGTTACATCAGCTTTGATTGGGGCAAGTCGTCCGCAACAAATGTTGAAAATGTTGC 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:1359"
/clone lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site=1: Smal; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial Alui digestion or by sonication.
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                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                1 (bases 1 to 3237)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci Aliments, (2002) In press

    .3237
    /organism="Lactococcus lactis subsp. cremoris"

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Rax: 33 1 34 65 25 21
Radl: GOTCKINGGJOUY.INTR.fr
Dest homologue in strain IL1403 is nadR (98*)
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                                                                              cremoris,
                                                                                                                  cremoria
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Location/Qualifiers
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Matches 287; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Score 84.6; DB 14;
48.2%; Pred. No. 3.3e-13;
                                                                                                               organism="Medicago truncatula"
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186 c
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Matches 237; Conservative
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RESULT 2 BH770958/c LOCUS DEFINITION

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DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN3TLO8 of DrosBAC library from Drosophila melanogaster (fruit
AL108460
                                                                   CNS01MQH 830 bp DNA linear GSS 14-JUN-2001 Anopheles gambiae GSS T7 end of clone 22E24 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 GGCGCTTCCACCTTGTTTGTCATGGCGTCTTTCGCTGCCATGACGGCAAACCATAACAGG 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1118 TAAGCGATGCCACCCCAGCGCATAATATCGAGCACGATCGGCGGCGCGTTGGACAAAAGA 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 AACGCCACGCCCCAGGTGACCAACGCCAGGAGCCACGGAGACTGCATCAGCAGCGCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission

Submitted (16-FRB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, Prance
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 GCCAGTICGAGGTIACTGCTCATCGCCGTTTTTCAGCGCGCCGAATCCGTACCAGAGCAGA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498 Arcarcagardenardecegandecertarirenteareceantringegeeee 557
                                                                                                                                                                                                                                                             Bukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.4; DB 17;
Pred. No. 4.2e-06;
1; Mismatches 137;
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/note="end : T7"
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/clone="22E24"
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/organism="Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                      - Web : www.genoscope.cns.fr)
2 (bases 1 to 830)
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                                                                                                                                                                                                                   African malaria mosquito.
                                                                                                                                enomic survey sequence.
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2.5%;
Best Local Similarity 50.7%;
Matches 142; Conservative 1
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CNS01MQH
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                                                                                                                                             AF075981 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 390-T3, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                    Wong, R.M.-Y., Wong, K.K., Benson, N.R. and McClelland, M. Sample sequencing of a Salmonella typhimurium LT2 lambda library: comparison to the Escherichia coli Kl2 genome FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 TGGAAAGGCTCTTTACGTGGGTATTTCTTCCTACGGTCCAGAGCTCACAGCGGAGGCGGC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 CATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAATGACATCGCCCAGGAACG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 TGAGTTCATGGCGGAGGAGGTGCCCGCTTCTGATTCATCAGCCAAGCTATTCCATCAT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGATATTCTGGAGGATCTCGGCACGCCTTGCCTGATTCATCAGCCTAAATATTCGCTTTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 TAATCGTTGGGTGGAACCGGGCGATGACGGTGAGAACTTGTTGCAGTCAGCTGCCAA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 17; Length 86
Pred. No. 1.8e-09;
0; Mismatches 160; Indels
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                             1991 AGCTTTAGAACGTCTGGAATTTACTGACGAAGAATT 1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifsci.sdsu.edu
535 TTCACTCAACAACTTGGAGTTTTCTGACGCCGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:602"
/clone="390-T3"
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                                                                                                                                                                                                                                                                           Salmonella typhimurium
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AF075981.1 GI:3320851
                                                                                                                                                                                                                                                                                                   Salmonella typhimurium
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Best Local Similarity 54.7%;
Matches 220; Conservative
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VERSION
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AUTHORS
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                                                                                                     RESULT 3
AF075981
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Direct Submission

Submitted (102-UJN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVIX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-ge and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and RST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
    Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR19D16"
                       Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                              REFERENCE
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                   Submitted (23-UTL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 GACGCCGAGTTGGAGGCGATCGATGAGATTTCCCACGACGCCGGCATCAACATTTGGGCG 619
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
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/clone lib="DrosBAC"
/plasmīd="pBeloBAC11"
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Drosophila melanogaster
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                             CGGTCATCACAACTGCCACGACGACGTTGATCCAGCGCCACACCTTGGGGGCTGGACAGCG 740
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   Length 925;
                                                                  Indels
/ Match 2.0%; Score 48.6; DB 17; Local Similarity 13.8%; Pred. No. 0.012; nes 49; Conservative 157; Mismatches 149;
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Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
                                                                                                                                                                                                                                                                                    Organism="Zea mays"
Cultivez="0H43"
(db xref="texon:4577"
Clone_lib="946 - tassel primordium prepared by Schmidt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Pred. No. 0.18;
0; Mismatches 176; Indels 0
                                                                                                                         Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                      986 TCAGTGGCCACCGCCGAACCGCCCAA 1011
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AL247708
AL247708.1 GI:7968720
GSS; genome survey sequence.
Tetraodon nigroviridis.
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Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="032806"
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48.2%; Pred. No. 0.18;
tive 0; Mismatches 129;
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Vector: pGAD10; Site: EGORI; GDNA library from fully
differentiated maize tissues from an active Mutator plant
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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T3 end of clone BB0AA013A11 of library BB0AA from strain CBS 4732
of Pichia angusta, genomic survey sequence.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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/cultivar="W23"
/db_xref="taxon:4577"
/clone lib="945 - Mixed adult tissues from Walbot lab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
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Fax: 650 725 8221
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AL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefegenoscope.cns.fr. | Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii. Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta. Bactis var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrvomya lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other attremity of this insert.
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Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
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Belotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrans, P., Lepingle, A., Libernete, B.,
Malpertuy, A., Neuvedise, C., Ozier-Kalogeropoulos, O., Porier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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Pred. No. 1.2;
); Mismatches 92;
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Submitted (08-SBP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 BYRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux. CP 5706, 91057 BYRY cedex, FRANCE. (E-mail:

Seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Muyveromyces hactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarromities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this ingert.
                                            CNS079WN 11near GSS 08-JUL-2001
T3 end of clone XBB0AA001G01 of library XBB0AA from strain CBS 4732
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similarity to aryl-alcohol dehydrogenases ]"
/evidence=not_experimental
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Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
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Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durens, P., Lephingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
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Matches 97; Conservative 0; Mismatches 92; Indels 0;
                                                                                        of Pichia angusta, genomic survey sequence.
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Rax: 319 335 9565
Rmail: msoarse@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequenciming by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequenciming by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequenciming by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequenciming by: Dr. M. Bento Soares, Univeristy of Iowa Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 143-166, >GC rich#Low_complexity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 558)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
223 CGTTATATTGGGGCCTCGACAATGAGGCTTATCAATTTATCGAAATGCAACATGTTGCT 282
                                                                                                                                                                                                                                                            283 GAAAAGCATGGTTGGACAAAGTTCCATTCCATGCAAAGCTATTATTCCCTGTTCTTCAGA 342
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Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Institute in Bufffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Prosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA linear GSS 03-JUN-15 brosophila melanogaster genome survey sequence T7 end of BAC #BACR14021 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                   644
                                                                                                                        260 ACATCGCCAACGAGGACTGCATCAAGGTGGCGGCCGTGCTCAACAACGCCTTCTACCTGG 319
                                                                                                                                                                     704
                                                                                                                                                                                                         320 AGAACCTGCACTTCACCATCGAGGGCAAGGACACGCACTACTTCATCAAGACCACCACGC 379
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 910)
                                                                                                                                                            AAAACTAACCCATCAACATCAGTTTGATGGCCÁATGCGGTCATCACAACTGCCACGACGA
                                                                                   585 AGATTTCCCACGACGCCGGCATCAACATTTGGGCGAAGGCCACCGATTCCAAAACCCGCG
                                                                                                                                                                                                                                                                                          AACCCACCAGGGGAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCGAAAATCCACC
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    Length 558;
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.7%; Score 41.2; DB 17;
Best Local Similarity 14.8%; Pred. No. 1.8;
Matches 47; Conservative 150; Mismatches 119;
                     Pred. No. 1.1;
0; Mismatches 145;
  DB 14;
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      Score 41.6;
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/note="end : T7"
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Query Match
Best Local Similarity 46.9%;
Matches 128; Conservative
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CNS006ON/c
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AUTHORS
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JOURNAL
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/dev_stage="fetal"
/lab_hos=="DH10B" (Life Technologies) (T1 phage resistant)"
/lab_hos=="DH10B" (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker: Site_1: EcoR I; Site_2: Not I;
U1-E-E01 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM729055 617 bp mRNA linear EST 01-MAR-2002
UI-E-EO1-aiw-a-06-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aiw-a-06-0-UI 5', mRNA sequence.
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Tel: 319 315 8260

Tel: 319 315 8260

Fax: 319 315 9565

Email: macares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655 SAVMAVAVAAASSAVASSGSSSVSCSSSRCGCSASSSSASSASSSSSSSSSSCGCGSC 596
                                    GTCGCCGTATTGCGCGCCGACGCCGCTGATAAACACGCGACGCGTCCAAATACGCATTCGG 891
                                                                                                                                                                                                                                                                                                                                                                                          892 GTTCAACCA--GGTCAGCACGATTGCCATCAACATGGGCTTTACCCAAACCCGCTGCTTA 949
CCAGCGCCACACCTTGGGGCTGGACAGCGGGCGTGACAATGCTGCTGCTGCGGAAACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          950 · TCGACGCTCACCTCCACCCGCACCCGGTTGCGCGTGTCAGTGGCCACCGCCGAACCGCCC
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Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="UI-E-EO1-aiw-a-06-0-UI"
/clone_lib="UI-E-EO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="fetal eye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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BM729055.1 GI:19050388
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Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
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mRNA sequence.
BE898495
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 770)

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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Liaboratory
CDNA Library Preparation: Ling Hong/Rubin Liaboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW819 row: p column: 23
High quality sequence stop: 765.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
constructed according to Bonaldo, Lennon and Soares
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/clone="TMAGE:3951622"
/clone=lib="MIH MGC 9"
/tissue_type="adenocarcinoma cell line"
                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 14; L
Pred. No. 1.8;
0; Mismatches 145;
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ilarity 46.9%;
Conservative (
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Matches 128;
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; CDNA made by oliqo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 245 c 277 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ACATCGCCAACGAGGACTGCATCAAGGTGGCGGCGCGTGATCAACAACGCCTTCTACCTGG 172
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0
                                                                                                                                                                                                                                                                                                                         1.7%; Score 41; DB 12; Length 770;
46.9%; Pred. No. 1.9;
ive 0; Mismatches 145; Indels
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Corynebacterium gl BCG deletion regio Mycobacterium tube Mycobacterium tube Corynebacterium gl Escherichia coli g Bacilus lichenifo E. coli DNA for ce E. coli DNA for ce

C glutamicum codin Salmonella typhi D Pseudomonas aerugi Genomic sequence o DNA encoding novel Lactobacillus rham

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Database

Result Š.

Escherichia coli y Klebsiella pneumon DNA encoding novel Genomic fragment # Stealth virus nucl Human breast cell Human foetal liver Probe #3471 for ge Human brain expres

Human bone marrow Probe #3489 for ge Probe #3604 used t Brobe #3437 used t Human genome-deriv Rice raffinose syn

Human cDNA sequenc Human cDNA sequenc Human cDNA sequenc Human breast cell

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LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
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AAH68419
AAF368077
AAF39683
AAF39682
AAF71729
AAF71729
AAF72786
AAS52558
AAAS59552
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AAAS565007
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/*tag= b
/label= LysE
complement (1723..2373)
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complement (82..954)
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ID AAT96816 standard; DNA; 2374 BP.
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/label= LysG
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/label= orf3
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C glutamicum codin
Corynebacterium gl
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10233.535 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 2374; Conservative
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                                                                                                                  WPI; 1997-333867/31.
P-PSDB; AAW37714-16.
                                                                                                                                                                                                                                          Corynebacterium
  22-DEC-1995;
                                                                             Eggeling L,
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                                                                                                                                                           ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGCGTCGATGGTCC
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                694 AATCCCGTTAACCATCGCCATCAACGCAGATTCGCTATCCACATGGTTTCCTCCCGTGTT
                                                                    634 CAACGAGGTAGCTTCTTGGGGTGGAGCAACGCTCACGCTGCGCTTGGAAGATGAAGCGCA
                                                                                                                  CACATTATCCTTGCTGCGCGTGGAGTGTTTTAGCAGCGGTAACCCGTGAAGCTAATCC
                                                                                                                                             CGTGGCGGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCACTTGGCCATTGCAACCCC
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                               C glutamicum coding sequence fragment SEQ ID NO: 7063
                 ВP
                AAH68528 standard; DNA; 349980
                                                                                        organic acid synthesis; ds
                                                                                                        Corynebacterium glutamicum
                                                (first entry)
                                                                                                                        EP1108790-A2
                                                26-SEP-2001
                                                                                                                                        20-JUN-2001
                               AAH68528;
RESULT 2
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541 CAACAACTIGGAGTITICIGACGCCGAGTIGGAGGCGAICGAIGAGAITICCCCACGACGC 600

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16-DEC-1999; 99JP-0377484. 07-APR-2000; 2000JP-0159162. 18-DEC-2000; 2000EP-0127688

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed execution, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 127595 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGCATGTTGCGTCTGGAAAGGC 127654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                              Yokoi
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Ikeda M, Ozaki A;
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                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                        Mizoguchi
Senoh A,
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                                                                          Nakagawa S,
Tateishi N,
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Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purline and pyrimidine bases

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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Metabolic pathway protein; MP; lysine biosynthesis pathway;
methionine biosynthesis pathway; large-scale production of fine chemical;
Corynebacterium diphtheriae; diphtheria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of novel Corynebacterium genes encoding metabolic pathway (MP) proteins (AAU71922). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polynucleotide sequences of the invention of expression of for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria.

AAS96073-AAS96132 represent C glutamicum genes encoding the novel metabolic pathway proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haberhauer G,
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                                                                                                                                                                                                                                                                                                                                                                                                           glutamicum gene #21 encoding metabolic pathway protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 993; DB 23;
100.0%; Pred. No. 2.6e-299;
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                                                                                                                                            2281 ATTGCGCCTTAGTTACTTCTGAAAAGGTTCAG 2313
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Conservative 0; Mismatches
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23-JUN-2000; 2000US-0606740.
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Best Local Similarity
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Matches 993;
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ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGCGTCGATGGTCC
                                                       661 ACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGGCGCGTCGATGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriam are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                            S, Hayashi M, Ochiai K, Yokoi
Ozaki A;
                                     amino acid synthesis; vitamin; saccharide;
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36.6%; Score 870; DB 22; Length 870;
Best Local Similarity 100.0%; Pred. No. 6.6e-261;
Matches 870; Conservative 0; Mismatches 0; Indels
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C glutamicum coding sequence fragment SEQ ID NO: 3456
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Ikeda M,
                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
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03-AUG-2000; 2000JP-0280988.
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2000JP-0159162.
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                                                    organic acid synthesis; ds.
                                                                                      Corynebacterium glutamicum
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Senoh A,
                                   Coryneform bacterium;
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P-PSDB; AAG93202.
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Tateishi N,
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301 ACAIGGTTTCCTCCCCGIGTTCAACGAGGTACTTCTGGGGTGGAGCAACGCTCACGCTG
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AAF71779 standard; DNA; 822 BP.
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99DS-0130476.
99US-0142101.
99DS-1031415.
99DE-1031418.
99DE-1031419.
99DE-1031420.
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases
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                                                                                                                           99DE-1031636.
99DE-1032125.
99DE-1032126.
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99DE-1032227.
99DE-1032228.
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03-SEP-1999
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Haberhauer

Zelder O,

Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;

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                                                                                       822 GATTCCAAAACCCGCGAAAACTAACCCATCAACATCAGTTTGATGGCCAATGCGGTCATC 763
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                               Gaps
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                                                         GATTCCAAAACCCGCGAAAACTAACCCATCAACTCAGTTTGATGCCCAATGCGGTCATC
                                                                                                                   ACAACTGCCACGACGTTGATCCAGCGCCACACCTTGGGGCTGGACAGCGGGCGTGAC
                                                                                                                                                                                             GCGGCGAAAATCCACCGTCCGGTGTCGCCGTATTGCGCCCCGCCGCCGCCGATAAACACA
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                                                                                                                                                                               749 AATGCTGCTGCGCCGAAACCCACCAGCGGAACCAGATCAGGCTTGCCGCGCAACGCGCCA
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 Length 822;
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    C. glutamicum gene #23 encoding metabolic pathway protein.

34.6%; Score 822; DB 22; Length 8. 100.0%; Pred. No. 6.5e-246; ive 0; Mismatches 0; Indels
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0uery Match
Best Local Similarity 100.0
Matches 822; Conservative
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methionine biosynthesis pathway; large-scale production of fine chemical; Corynebacterium diphtheriae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel Corynebacterium glutamicum genes encoding metabolic pathway (MP) proteins of AMU71863-AAU71921). The metabolic pathway proteins of the invention include enzymes involved in the lysine and methionine biosynthetic pathways. The polynucleotide sequences of the invention can be used for the large-scale production and/or modulation of expression of fine chemicals such as lysine and methionine. The sequences of the invention may be used to identify C. glutamicum and related organisms e.g. C. diphtheriae in a subject to detect diphtheria.

AAS96073-AAS96132 represent C. glutamicum genes encoding the novel metabolic pathway proteins of the invention.
                                                                                                                                                                                                                                      Kim J;
                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding metabolic pathway proteins from Corynebacterium glutamicum, useful for producing methionine and lysine in Corynebacterium and Brevibacterium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGCGTCCAAATACGCATTCGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGC
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                                                                                                                                                                                                                                   Schroeder H, Zelder O, Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.6%; Score 822; DB 23; Length 822; 100.0%; Pred. No. 6.5e-246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;
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Matches 822; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 214-215; 316pp; English.
                                                                                                                             22-DEC-2000; 2000WO-IB02035
                                                                                                                                                          09-MAR-2000; 2000US-187970P.
23-JUN-2000; 2000US-0606740.
                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                     B,
                                                                                                                                                                                                                                   Kroeger
                                                                                                                                                                                                                                                                          WPI; 2001-582269/65.
                                                                                                                                                                                                                                                                                          P-PSDB; AAU71888
                                                                                                                                                                                                     (BADI ) BASF AG.
                                                                                                                                                                                                                                                    Hwang B;
                                                                       W0200166573-A2
                                                                                                  13-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
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                                                                                                                    222 ACGAGAAGAACCCCCAATGAGTCCTTCGTTAATTCCTTGTTTAATCACCAGTACATTC
1049 ATGATCTGTGGCGCTTCCACCTTGTTTGTCATGGCGTCTTTCGCTGCCATGACGGCAAAC
                        1169 GACAAAAGATCAACGCCCAAGGTGCCGGCGATGAACAAAAAGACGTCAGAAATTAAACAC
                                                                                                                                                                                                                  1229 ACGAGAAGAACCGCAATGAGTCCTTCGCGCTTAATTCCTTGTTTAATCACCAGTACATTC
                                                                                                                                                                                                                                                                                                                                                                                1289 IGCGGTCCGATGGACAGTAAAAGACTGGCCCCCCAAAAGCAGACCTGTAATGAAGATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                              ATGATCACCATCGTGACCTATGGAAGTACTTAAGTAAAATGATTGGTTCTTAACATGGTT
                                                                                           Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 3455; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum coding sequence fragment SEQ ID NO: 3455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAATATAGCTTCATGAACCCCATTCAACTGGACACTTTGCTC 1450
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H, Ando S
Ikeda M,
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thermoaminogenes lysin biosynthetic enzyme lysE DNA

Heat-resistant; lysin biosynthesis; enzyme; aspartate-semialdehyde dehydrogenase; lysE;

Corynebacterium thermoaminogenes

JP2001120270-A

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mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, asccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 CAGCGGGAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCGAAATCCACCGTCCGGT
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                                                                                                                                                                                                                                                                    29.8%; Score 708; DB 22; Length 708; 100.0%; Pred. No. 2.6e-210; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                Sequence 708 BP; 134 A; 173 C; 221 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                         Local Similarity 100.
1es 708; Conservative
                                                                                                                                                                                                                                                                                                            Matches 708;
                                                                                                                                                                                                                                                                    Query Match
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(first entry)

11-SEP-2001

AAH45375;

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A heat-resistant lysin biosynthetic system enzyme gene of a high

temperature-resistant coryneform microbe

WPI; 2001-364760/38. (AJIN) AJINOMOTO

P-PSDB; AAG64047

99JP-0311148 99JP-0311148

01-NOV-1999; 01-NOV-1999;

08-MAY-2001.

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C glutamicum coding sequence fragment SEQ ID NO: 3454

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The present invention provides a number of nucleotide and protein agequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, cor expression pattern of a gene derived from coryneform bacterium, coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, accommendation of a gene derived from coryneform bacterium, saccharides and organic acids, particularly 1-1ysine. The present sequence is a nucleic acid described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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AAH68419 standard; DNA; 627

RESULT 10

26-SEP-2001 (first entry)

AAH68419;

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GAACAATATTGATATGGTCCGCAAGCTCAATGACATCGCCCCAGGAACGCGGGCAGTCACT
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Matches 499; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
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           AGCCAGGGTAAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGC
                                                      AAGCTCAATGACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCGTGA
                                                                                                   TCGTCAGTTGAGCAGCTGGACAACAGCCTTGATTCACTCAACAACTTGGAGTTTTCTGAC
                                                                                                                                                                         GCCGAGTTGGAGGCGATGAGATTTCCCACGACGCCGGCATCAACATTTGGGCGAAG
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<u> AGCCAGGGTAAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGC</u>
                                           AAGCTCAATGACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCATGG
                                                                                     Corynebacterium glutamicum MCT protein encoding DNA SEQ ID NO:669
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09-JUL-1999;
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27-AUG-1999;
27-AUG-1999;
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Gaps 9

20.4%; Score 485.2; DB 22; Length 993; 99.0%; Pred. No., 1.4e-140; ive 0; Mismatches 3; Indels 2;

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609 180 699 729 300 789 849

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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AABF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
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99DE-1040831.
99DE-1040832.
99DE-1040833.
99DE-1041379.
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P-PSDB; AAB76844.
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27-AUG-1999;
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31-AUG-1999;
31-AUG-1999;
03-SEP-1999;
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03-SEP-1999;
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CTTTCCATTTCCCCCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGT 1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region regulars in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT3537) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an orithment, or a virulent, mycobacterial phenotype. Determination of a virulence, or avirulents the detection of the presence or absence of the deletion; the deletions are detected either by detecting the contained within the deletion. Deletion junctions (see AAT3538-46), or by detecting the presence or absence of absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACTGGACACTTTGCTCTCAATCATTGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCC 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5253 CAGCTGCCGCATTGCCTGCCGTCGAACTGGGCAGCTTCGATGCGGCCGCGGAGCGC 5312
910 TGCGCAGATGGCGCTTGCATGGGTGCTGCGCGAGCAAAGAGAGTACGGCGCCCGGATTACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               petecting markers for avirulence in Mycobacterium - used in
production of vaccines against bacterial infection, and to detect
bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%; Score 122.8; DB 17; Length 15239; ilarity 49.7%; Pred. No. 1.5e-26; Conservative 0; Mismatches 422; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene deletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15239 BP; 2878 A; 4791 C; 4729 G; 2841 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
3382..14071
/*tag= a
/note= "BCG delta 1 deletion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    delta 2; virulence; avirulence; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                      BCG deletion region 2 and flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mycobacteria; vaccine; infection; marker; ss.
                                                                                     970 GTGACCAGTGCATTGATTGGTGCT 993
                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium bovis strain BCG
                                                                                                                                                                                                                                                           AAT33536 standard; DNA; 15239
                                                          479 GTGACCAGTGCATTGATTGGTGCT
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Best Local Similarity
Matches 434; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mahairas GG,
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                                                                                                                                                                                                    RESULT 12
AAT33536
ID AAT3
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2143 5963

5903

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6024 TATTGGCAATGCTGGAACTGGACAGTCCGATCATCGCGCGAATTACCGACGCGTGAGG 6083 Mycobacterium tuberculosis, strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO US6294328-B1.

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2226461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 2227112 CTACATGTCACCCGTCGGCTGTCAGTCAGCGCATCAAGTCGTTGGAGCAGCAGGTCGGC 2227053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 2227052 CAGGTGCTGGTGGTCAGGGAAAAGCCATGTCGGGCGACGACGACGCAGGTATCCCGGTGTTG 2226993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2226932 GCGTCGCTGAACGCACGCGGATCACCATTGCGGTAAACGCCCGATTCCATGCCGACATGG 2226873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 2226761 ACCGAGCGGAACCCGGTGCCGGGCTGCCGGGTGCACCCGCTGGGTGAAATGCGCTACCTA 2226702
                                                                                                                                                                                                                                                                                                                                          The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the mucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1727 ITTCCTCCCGTGTTCAACGAGGTAGCTTCTTGGGGTGGAGCAACGCTCACGCTGCGCTTG 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1433 CAACTGGACACTTTGCTCTCAATCATTGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCC 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1493 CTTTCCATTTCCCCCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGT 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1553 CGAGTGTTGGTATCGCGCACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTG 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1613 CAAGCAGCGCGGAAAATGGTGTTGCTGCAAGCAGAAACTAAAGCGCAACTATCTGG--AC 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1787 GAAGATGAAGCGCACACATTATCCTTGCTGCGCGTGGAGATGTTTTAGGAGCGGTAACC 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1847 CGTGAAGCTAATCCCGTGGCGGGATGTGAAGTAGTAGAACTTGGAACCATGCGCCACTTG 1906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1671 GCCTTGCTGAA----ATCCCGTTAACCATCGCCATCAACGCAGATTCGCTATCCACATGG 1726
                                                                                                                                                                                                                    Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.1%; Score 121.2; DB 22; Length Best Local Similarity 49.5%; Pred. No. 1.7e-24; Matches 433; Conservative 0; Mismatches 423; Indels
                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English
                                                                                                                                                    Venter JC;
                                                                                                                                                      Fraser CM,
                                                98US-0103840
                                                                                 98US-0103840
                                                                                                                                                    Fleischmann RD, White OR,
                                                                                                                    GENOMIC RES
                                                                                                                                                                                                                                                                          1551 and H37Rv differ
                                                                                                                                                                                   WPI; 2001-647261/74.
                                                24-JUN-1998;
                                                                                                                    (GENO-) INST
                                                                                 24-JUN-1998;
                25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monitoring.
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2226701 CCAGTGGCCAGCCAGCCATCGTCGACGGCCATCTATCCGACGGGTTCACTGCCGCCGCG 2226642
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                                                                                                                                                                                                           2226641 GCGGCTAAAGCTCCGTCACTGGCGTGGAATCGTGACGATGGGCTGCAGGACATGTTGGTG 2226582
                                                                                                                                                                                                                                                                                                                                                                                   2226581 CGTAAGGCCTTTCGTCGCGCCATCACCAGACCGACGTTTGTCCCCGACACACAGAGGC 2226522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCCGCTTGCCGATGGATCGTTCGTACGCGTCTGCGACATACACCTCGACGTCCCTCTC 2226402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2084 TTTGGTGAGGCAATTCGCCGAGGCCTTGGTTGGGGACTTCTTCCCGGAAACCCCAAGCTGCT 2143
                                                                                                                           1967 GCGATGCCCGTCTTACGCTTCGGTCCCAAAGATGTGCTTCAAGACCGTGACCTGGACGGG 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2226341 GCGGCGGCAAGCGGTCTGTACCGGGGCCAGCAAC 2226308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI99682 standard; DNA; 4411529
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AAF71729 standard; DNA; 1200

(first entry)

30-APR-2001

AAF71729;

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                                                                                                                                                                                                                                                                                                                                         2229753 CAGGIGCIGGIGGICGICAAAAGCCAIGICGGGGGACGACGACGCAGGIAITCCCGCIGIIG 2229694
                                                                                                                                                                                                                                                                                                                                                                                                            2229633 GCGTCGCTGAAACGCACGCGGATCACCATTGCGGTAAACGCCGATTCCATGCCGACATGGC 2229574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 2229402 ccadrodechaceaegechrecaececertrareceaedaceaerreaeraecececeeege 2229343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2229282 GGTAAGGCCTTTCGTCGCGCCATCACCAGACGGACGCACTTTGTCCCGACCACAGAGGGC 2229223
                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                               Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                            1493 CITICCATTICCCCCTCGGCGGTGAGTCAGCGGGTTAAAGCTCTCGAGCATCACGTGGGT 1552
                                                                                                                                                                                                                                                                                                           1553 CGAGTGTTGGTATCGCGCACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTG 1612
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                                                                                                                                                                               CAACTGGACACTTTGCTCTCAATCATTGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCC 1492
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                                                                                                                Score 121.2; DB 22; Length 4411529;
Pred. No. 1.7e-24;
0; Mismatches 423; Indels 18; Ga
                                                 at segdata.uspto.gov/sequence.html?DocID=6294328B1.
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RESULT 15

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Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:739.
                                                                      SMP protein, sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleoside; nucleoside; atty acid; unsaturated fatty acid; unsaturated fatty acid; arbohydrate; aromatic compound; vitamin; cofactor; polyketide; elzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
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or
                                                  Corynebacterium glutamicum; carbon metabolism and energy production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
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cenergy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a coffect a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a coffactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corprebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing the undicative and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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Sequence 1200 BP; 272 A; 367 C; 294 G; 267 T; 0 other;

ö Query Match
4.3%; Score 101; DB 22; Length 1200;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 101; Conservative 0; Mismatches 0; Indels 0

2334 GCAGGAATTGGGCCAGGCAGAGTAACACCTTCAGCAAATGG 2374 ઠ 셤

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1140 GCAGGAATTGGGCCAGGCAGAACACCTTCAGCAAATGG 1100

Search completed: April 27, 2003, 02:57:01 Job time : 10751.4 secs

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2: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 77, Appl Sequence 6195, Ap Sequence 1395, Ap Sequence 9644, Ap Sequence 4130, Ap Sequence 15, Appl Sequence 15, Appl Sequence 11, Appl Sequence 3471, Ap Sequence 142, App Sequence 19241, A Sequence 2513, Ap Sequence 47, Appl Sequence 3456, Ap Sequence 3455, Ap Sequence 3455, Ap Sequence 3454, Ap Sequence 12, Appl Sequence 1, Appli Description US-09-746-660A-47 US-09-738-626-3456 US-09-738-626-3455 US-09-738-626-3455 US-09-738-626-3455 US-09-738-626-3455 US-09-738-626-3454 US-09-738-626-135 US-09-811-242-6195 US-09-815-242-644 US-09-815-242-9644 US-09-815-242-9644 US-09-815-242-9644 US-09-815-242-9644 US-09-815-242-7643 US-09-894-844-11 US-09-864-761-3471 US-10-114-170-142 US-09-864-761-19241 US-09-864-761-2513 Query Match Length DB 1879 1075 1403 Score 42.8 40.4 40.4 121.2 93.2 82.6 78 57.6 76. Result No. υ υu

Db 1327595 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTTGCGTCTGGAAAGGC 1327654

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Query Match
100.0%; Score 2374;
Best Local Similarity 100.0%; Pred. No. 0;
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٠.	APPLICANT			HI, HIROSHI	SHI		
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٠.	APPLICANT		OCHIAI.	KEIKO			
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          1561 GGTATCGCGCACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTGCAAGCAGC
                                                 241 GGTATCGCGGACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTGCAAGCAGC
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: AVONO, HARUHKO
APPLICANT: YOKOI, HARUHKO
APPLICANT: TATEISHI, NAKOO
APPLICANT: TATEISHI, NAKOO
APPLICANT: TREDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENE: 249-125
CURRENT FILING DATE: 2000-12-18
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2281 ATTGCGCCCTTAGTTACTTCTGAAAAGGTTCAGGGTTTTTCACTT
                                                                                                                                                                                                                                                                                                                                                           Sequence 47, Application US/09746660A
Publication No. US20030049804A1
GENERAL INPORMATION:
APPLICANT: Pompelus, Markus
APPLICANT: Schroder, Harkus
APPLICANT: Schroder, Harkus
APPLICANT: Application Cokar
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CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
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; OTHER INFORMATION: RXA01393
US-09-746-660A-47
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PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FLING DATE: 1999-12-16

PRIOR PLING DATE: 1909-12-16

PRIOR PLING DATE: 2000-04-07

PRIOR PLILING DATE: 2000-08-03

PRIOR PLILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SEQ ID NO 3456

LENGTH: 870
                                                                                                                                                                                               ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-3456
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APPLICANT: Handerhauer, Gregor
APPLICANT: Handerhauer, Gregor
APPLICANT: Handerhauer, Gregor
APPLICANT: Handerhauer, Gregor
TITLE OF INVENTION: CONVERBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121072
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-08-12
PRIOR FILING DATE: 1909-07-08
NUMBER OF SEQ ID NOS: 125
SEQ ID NO 51
LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101).. (799)
LOCATION: (101).. (799)
US-09-746-660A-51
                                       841 GTTGATGCAGCAATCGAGGATTGCGGCCT
2261 GTTGATGCAGCAATCGAGGGATTGCGGCCT
                                                                                                                                                                                                                                    Sequence 51, Application US/09746660A Publication No. US20030049804A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
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Conservative

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Matches 708;
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Publication No. US20020197605A1
GERREAL INFORMATION:
APPLICANT: NAKGARA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAVASHI, MIKIRO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TEEDA, MASHTO
APPLICANT: TEEDA, MASHTO
APPLICANT: TEEDA, MASHTO
APPLICANT: OZAKI, AKID
ITILB OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-16
FRIOR APPLICATION NUMBER: JP 00/159162
FRIOR PILING DATE: 1999-12-16
FRIOR PILING DATE: 2000-04-07
FRIOR PILING DATE: 2000-04-07
FRIOR APPLICATION NUMBER: JP 00/280988
FRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn Ver: 3.0
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US-09-738-626-3455
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29.8%; Score 708; DB 9; Length 708; 100.0%; Pred. No. 3.4e-230;

Query Match Best Local Similarity

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   Gaps
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   Mismatches
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APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AXIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TILE REPRENCE: 249-125
CURRENT FILING DATE: 200-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YEMSHI, NAOKO
APPLICANT: SENOH, AKTHIRO
APPLICANT: IKEDA, MASATO
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Best Local or...
Matches 433;
                                                                                                           LENGTH: 909
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APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species of TITLE OF INVENTION: the M. Tuberculosis Complex
FILE REFERENCE: STAN102CON
CURRENT APPLICATION NUMBER: US/09/894,844
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Best Local Similarity 100.0%; Pred. No. 1.2e-202;
Matches 627; Conservative 0; Mismatches n.
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                                                                                                       ORGANISM: Corynebacterium glutamicum
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Sequence 12, Application US/09894844
Patent No. US20020176873A1
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin Ver. 3.0
SOFTWARE: Patentin Ver. 4.0
LENGTH: 627
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Pred. No. 3.8e-30;
0; Mismatches 423;
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.05
LIDNO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-12
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Conservative
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APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION UNDERS: US/09/974,300
CURRENT PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
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56.0%; Pred. No. 1.4e-20;
iive 0; Mismatches 173;
2264 GATGCAGCAATCGAGGGATTGCGGCCTTAGTTAC 2297
                                                                                             859 GCGCCGCCAAGCCGTCTGTACCGGGGCCAGCAAC 892
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Sequence 6195, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                          Sequence 77, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
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; ORGANISM: Bacillus licheniformis
US-09-974-300-77
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Matches 251; Conservative
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Best Local 8
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Ohlsen, Kari L.

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1515 TGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGTCGAGTGTTGGTATCGCGCCACCC 1574
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Pred. No. 5.3e-17;
0; Mismatches 234; Indels
                                                                                                                                                                           APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6195
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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ORGANISM: Escherichia coli
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; LOCATION: (1)...(894)
US-09-815-242-6195
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ'ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9644
                                                                                                                                                            TYPE: DNA
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                               , LOCATION: (1)...
US-09-815-242-9644
                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
                                                                                                                                             LENGIH: 894
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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1. 2.2e-15;
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100.0%; Pred. No....
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                            TLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 00/159162
RIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1395
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                  Sequence 1395, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1395
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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APPLICATION NUMBER: 60/207,727
ALING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/253,625
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
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                                                                                     APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                Gaps
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                 Length 894;
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Score 76.2; DB 10;
Pred. No. 8e-15;
0; Mismatches 413;
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        3.2%;
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IITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Method-
IITLE OF INVENTION: Using Them
                                                                                                                                                                         1889 GGAACCATGCCCCACTTGCCATTGCAACCCCCTCATT-----GCGGGATGCCTACATG 1942
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CURRENT APPLICATION NUMBER: US/09/971,536

CURRENT PILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238

PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623

PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623

PRIOR FILING DATE: 2000-11-28

PRIOR PLING DATE: 2000-11-28

NUMBER OF FLING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0

FRIOR PLING DATE: 2001-08-08

CONTWARE: PASTSEQ FOR WINDOWS VERSION 4.0
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Pred. No. 1.5e-10;
0; Mismatches 270; Indels
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Patent No. US20020159976A1
GENERAL INFORMATION:
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Matches 279; Conservative
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O'Toole, Paul
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US-09-971-536-15
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3.1%; Score 73; DB 10; L.
Best Local Similarity 46.0%; Pred. No. 9.9e-14;
Matches 413; Conservative 0; Mismatches 460;
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CURRENT FILING DATE: 2001-03-21
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PPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of
ITLE OF INVENTION: Prokaryotes
ILE REFERENCE: ELITRA.011A
                                                                                                   Sequence 4130, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
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US-09-815-242-4130
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APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Carr, Grant J.
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TGGGTATTTCTTCCTACGGTCCAGAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGG 128
                                          s68 irogiairirccaacirargaracgaagcagaccaaagaagcaarrigcgargriraaagarc 727
                                                                                             129 AGGGCTGCCCGCTTCTGATTCATCAGCTATTCCATCATTAATCGTTGGGTGGAGG 188
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 00/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2001-02-16
WUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO,7643
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Patent No. US20020061569A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
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Zyskind, Judith W.
Wall, Daniel
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Pred. No. 1.6e-08;
0; Mismatches 414;
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Patent No. US20020176873A1
GENERAL INFORMATION:
APPLICANT: Sehr, Marcel
APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 44.2%;
Matches 335; Conservative
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; LOCATION: (1)...(762)
US-09-815-242-7643
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## APPLICANT: Wilson, Michael A.

### TITLE OF INVENTION: Molecular Differences Between Species of TITLE OP INVENTION: the M. Tuberculosis Complex FILE REFERENCE: STAND 2000M

### CURRENT APPLICATION NUMBER: US/09/894,844

### CURRENT FILING DATE: 2001-06-27

### PRIOR FILING DATE: 1999-05-25

### PRIOR FILING DATE: 1998-05-25

### PRIOR FILING DATE: 1998-06-55

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Search completed: April 27, 2003, 06:55:06 Job time : 5075.11 secs

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(without alignments)
5443.169 Million cell updates/sec
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Sequence 20, A
Sequence 142,
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Sequence 2,
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                                                                                                   April 26, 2003, 20:22:28 ; Search time 133.755 Seconds
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-920-827-20
US-08-921-177-20
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US-08-920-828-20
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JS-09-134-001C-928
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US-09-103-840A-2
US-09-103-840A-1
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Listing first 45 summaries
                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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sednence 3, 1	Sequence 3, Appl	Sequence 27,	Sequence 27,	Sequence 27,	Sequence 940,	Sequence 1, Appli	ะก	22	Sequence 5, Appl	-1	Sequence 28,	Sequence 28,	Sequence 1, Appl	Sequence 18,	Sequence 18,	Sequence 1, Appl	22
US-07-642-734C-3	US-08-439-009A-3	US-08-205-697A-27	US-08-702-525-27	PCT-US95-02576-27	US-08-998-416-940	US-08-147-772-1	US-08-456-104-5	US-08-101-624-22	US-08-751-767A-5	US-08-153-262-1	US-08-479-744A-28	US-08-280-757B-28	US-09-159-135-1	US-08-205-697A-18	US-08-702-525-18	US-09-450-798-1	US-09-326-186B-225
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33.2	33.2	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
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ALIGNMENTS

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5253 CAGCTGGCCGCATTGGCTGCCGTGGTCGAACTGGGCAGCTTCGATGCGGCCGCGGAGCGC 5312
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Sequence 17, Application US/08390878

Septent No. 570060803

GRNERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 422;
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REGISTRATION NUMBER: 38,498
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TELECOMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Matches 434; Conservative
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                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
COUNTRY: USA
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STRANDEDNESS:
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         US-08-390-878-17
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1433 CAACTGGACACTTTGCTCTCAATCATTGATGAAGGCAGCTTCGAAGGCGCCTCCTTAGCC 1492 Gaps

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1612
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                                                        5313 CTACATGTCACCCCCTCGGCTGTCAGTCAGTCGTTGGAGCAGCAGGCGGC
    CTTTCCATTTCCCCCCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGT
                                                                                                                                                                    CGAGTGTTGGTATCGCGCACCCAACCGGCCAAAGCAACCGAAGCGGGTGAAGTCCTTGTG
                                                                                                                                                                                                                                                                                                                                    CAAGCAGCGCGGAAAATGGTGTTGCTGCAAGCAGAAACTAAAGCGCAAACTATCTGG--AC
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RESULT 2
US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 629432B
; GENERAL INFORMATION:
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: WINTER, John C.
ITLLE OF INVENTION: DAM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITLLE OP INVENTION: DAM SEQUENCES
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER, OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
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Db 2227172 CAGCTGCCGCTGCCGTCGAACTGGGCTACTAGGTTCGATGCGGCCGCAGGGC 2227113
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                                                                                                                                                                                                                                                                                                                                                                                                                        1433 CAACTGGACACTTTGCTCTCAATCATTGAAGGCAGCTTCGAAGGCGCCTCCTTAGCC 1492
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                                                                                                                                                                                                                                                                                                Length 4403765
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                                                                                                                                                                                                                                                                                                Score 121.2; DB 4;
Pred. No. 7.1e-24;
0; Mismatches 423;
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                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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                                                                                                                FRATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.51
Matches 433; Conservative
                            4403765
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SEQ ID NO 2
LENGTH: 44
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Db 2229873 CAGCTGGCCATTGGCTGCCTGGTCGAACTGGGCAGCTTCGATGCGGCCGCGGGGGC 2229814
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                                                                                                                                                                    APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
WUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
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5.1%; Score 121.2; DB 4; Length
Best Local Similarity 49.5%; Pred. No. 7.1e-24;
Matches 433; Conservative 0; Mismatches 423; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHEN: INFORMATION: H37Rv
US-09-103-840A-1
                                   Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4411529
-09-103-840A-1/c
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Db 2229102 TATTGGCAATGCTGGAAACTGGACAGTCCGATCATCGCGCGAATTACCGACACGGCGGG 2229043
                                          Db 2229162 rcrccgcrrgccgardgarcgrrcgracgcarcracgacaracacacacacaccrcgacgrcccrcrc 2229103
2084 TITIGGIGAGGCAATTCGCCGAGGCCTTGGTTGGGGACTTCTTCCCGAAACCCAAGCTGCT 2143
                                                                                                                                                                                        1 AGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGTGTGCGTCTGGAAAGGC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Saars Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: Illinois COUNTRY: United States of America ZIP: 6060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPA: DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/920,812 FLING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
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Similarity 50.5%; Pred. No. 1.7e-19;
36; Conservative 0; Mismatches 332;
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                                                                                                                                                                                                                                                                                     2264 GATGCAGCAATCGAGGGATTGCGGCCTTAGTTAC 2297
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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Clinical Isolate EC-625
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Patent No. 5763188
GENERAL INFORMATION:
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APPLICANT: Matsuhisa, Akio
APPLICANT: Ushara, Hirotsugu
APPLICANT: Eda, Soji
IITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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TELEFAX: 312/474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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LENGTH: 5541 base pair
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STRANDEDNESS: double
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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US-08-920-812-20/c
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Best Local Simi
Matches 386;
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US-08-920-812-20
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3416 AAATACGCCGATGGAAGAAACCGCCTCTGCGCTGGCTCATGCGGTACAAAGCGGTAAGGC 3357
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                                             61 TCTTTACGTGGGTATTTCTTCCTACGGTCCAGAGCTCACAGCGGAGGCGGCTGAGTTCAT
                                                                                          3356 GCTTTATGTCGGGATCTCCTCTTACTCGCCAGAGCGGACGCAAAAATGGTTGAGTTGCT
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Patent No. 5770375
GENERAL INFORMATION:
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
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3131 CATTCCGCAAGATTCACGGATGCATCGTGAAGGGAATAAAGTTCGTGGTCTGACGCCGAA 3072
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PatentIn Release #1.0, Version #1.25
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Pred. No. 1.7e-19;
0; Mismatches 332;
                                                  APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AMC-1997
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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US-08-920-827-20
                                                                                                                                                                                                                                                       NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
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TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
IENGTH: 5541 base pairs
"WPE: nucleic acid
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1 FELECOMMUNICATION INFORMATION
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Best Local Similarity 50.5%;
Matches 386; Conservative
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                         CURRENT APPLICATION DATA
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ORIGINAL SOURCE:
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GGCGGAGGAGGACTGCCCGCTTCTGATCAGCCAAGCTATTCCATCATTAATCGTTG 180
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US-08-362-577C-20/c
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APPLICANT: Matsubisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                2730 AGCCCÁTCACAAATGCAGAGAGCACAAACGTCAGATGATAATG 2687
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
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4.2%; Score 100.8; DB 1;
Best Local Similarity 50.5%; Pred. No. 1.7e-19;
Matches 386; Conservative 0; Mismatches 332;
COUNTRY: United States of America ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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STRAIN: Clinical Isolate EC-625
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Patent No. 5798211
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REGISTRATION NUMBER: 33,547
REFRENCE/DOCKET NUMBER: 1903
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-648
TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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STATE: Illinois
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US-08-921-177-20/c
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US-08-921-177-20
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3296 GCGCGAGTGGAAAATTCCGCTGTTAATTCATCAACCTTCGTACAATTTACTGAACCGCTG 3237
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Batent No. 5807673

GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Ghara, Hirotsugu
APPLICANT: Eda, Soji
ITILE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 27-MAR.1995
CLASSIFICATION: 536
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4.2%; Score 100.8; DB 1;
Best Local Similarity 50.5%; Pred. No. 1.7e-19;
Matches 386; Conservative 0; Mismatches 332;
                                                           19036/32420
                                                                                                                                                                                                                                                                                                                                                                                         , UKGANISM: BECherichia coli
; STRAIN: Clinical Isolate EC-625
US-08-362-577C-20
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 190:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
TELEPAX: 312/474-648
TELEX: 25.3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
TENGTH: 5541 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AATTCCAGAGGGTTCCCG--
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                                                                                                                                                                                                                                                                                                                   Probe for Diagnosing Infectious Disease
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2730 AGCCCATCACAAATGCAGAGGGCACAAACGTCAGATGGATAATG 2687
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPACIBLE
CORFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100.8; DB 2;
Pred. No. 1.7e-19;
0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFRENCE/DOCKET NUMBER: 19036/32420
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-625
US-08-920-828-20
                                                                                                                                           Sequence 20, Application US/08920828
Patent No. 5853998
                                                                                                                                                                                                             APPLICANT: Ohno, Teuneya
APPLICANT: Mateuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.5%;
Matches 386; Conservative
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5541 base pairs
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STRANDEDNESS: double
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STREET: 630.
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                                                                                             RESULT 8
US-08-920-828-20/c
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; LOCATION:
US-08-492-027A-9
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241 TGGCGTCATTGCTTTCTCACCACTTGCGCAGGGCCTGCTCACGGACAAATATCTCGATGG
                                                    3191 GGGCTGTATTGCCTTTACTCCTCTGGGGATTGCTGACGGAAAATATCTCAACGG
                                                                                                           301 AATTCCAGAGGGTTCCCG------CGCCAGCCAGGGTAAGTCCCTGTCTGAGGG
                                                                                                                                                                                                                   349 CATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAATGACATCGCCCAGGAACG
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2730 AGCCCATCACAAATGCAGAGAGCACAAACGTCAGATGGATAATG 2687
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT >
US-09-453-702B-142
US-09-453-702B-142
Sequence 142, Application US/09453702B
Fatent No. 6365723
GENERAL INFORMATION:
Hattner, Frederick R.
BULICANT: Blattner, Valerie
BULIAND, Valerie
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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54.4%; Pred. No. 0.015;
(ve 0; Mismatches 72; Indels 0
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Sequence 9, Application US/08492027A
Sequence 9, Application US/08492027A
Sequence 9, Application US/08492027A
SEQUENCE 110 Sequence 1
SEQUENCE 10 Sequence 1
SEQUENCE 10 SEQUENCE 9
CORRESPONDENCE 9
CORRESPONDENCE 1 SEQUENCE 1
STREET: PO. Box 747
STREET: Falls Church
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/492,027A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-206
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1329 TAAGTCAGGCAATTGCTGCCCTCGAACAAGAACTTGGT 1366
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                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-09-453-702B-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
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COUNTRY: USA
ZIP: 22040-0147
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC COMPATIBLE
                 (608) 251-9166
TELEFAX: (608) 251-91
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%;
Best Local Similarity 54.4%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1935 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..1638
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Patent No. 629438

GENERAL INFORMATION,
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 720208 GCCATCGACGCGGTAAACCCGTGCAACGCGTTGTGGCCGCGACCGGGGCCGATCTCCCCG 720267
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                                                                                                                        Gaps
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                                                                                                                                                                                                                      520 GGACAACAGCCTTGATTCACTCAACAACTTGGAGTTTTTCTGACGCCGAGTTGGAGGCCGAT
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               Length 1935;
          Score 39.6; DB 2; Length 1
Pred. No. 0.14;
0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1443 GATGAAGGTAAAGAAAGAGCACGCCTCGGTGCCG 1476
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               1.7%;
Query Match
Best Local Similarity 49.19
Matches 105; Conservative
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US-09-103-840A-2
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Sequence 1, Application US/09103840A Patent No. 6294328

RESULT 12 US-09-103-840A-1

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Db 718775 GCCATCGACGCGGTAAACCCGTGCAACGCGTTGTGGCCCGCGACCGGGCCGATCTCCCCG 718834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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Patent No. 5608147
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: tfdA Gene Selectable Markers in Plants and the TITLE OF INVENTION: Use Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755 GCTGCGCCGAAACCCAACCAGCGGAACCAGATCAGGCTTGCCGCGAACGCGCCAGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy. 875 TCCAAATACGCATTCGGGTTCAACCAGGTCAGCACGATTGCCATCAACATGGGCTT 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.6; DB 4; Length 4 Pred. No. 34; 0; Mismatches 124; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.6%;
Best Local Similarity 47.5%;
Matches 112; Conservative
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CLASSIFICATION: 800
                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
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US-08-358-117-1/c
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LENGTH: 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1493 CITICCALITICCCCCTCGGCGGTGAGTCAGCGCGTTAAAGCTCTCGAGCATCACGTGGGT 1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TIMMIS, KENNETH N.
APPLICANT: TIMMIS, KENNETH N.
APPLICANT: TIMMIS, KENNETH N.
APPLICANT: TIMMIS, KENNETH N.
APPLICANT: TIMMIS, KENNETH N.
TITLE OF INVENTION: 2,4-DICHLOROPHENOXYACETIC ACID (2,4-DICHLOROPHENOXYACETIC CID (2,4-DICHLOROPHENOXACE
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,588
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGRNT INFORMATION:
NAWE: LAWRENCE, WILLIAM F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514413-3526
TELECOMMUNICATION INFORMATION:
TELEFACHION: 212-588-0500
TELEFACK: 212-588-0500
TELEFACK: 212-588-0500
                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1;
Pred. No. 0.83;
0; Mismatches
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Patent No. 6100446
GENERAL INFORMATION:
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TELEFAX: 212-588-0500
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2058 base pairs
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Best Local Similarity 53.9%;
Matches 76; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 2058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
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STRANDEDNESS: single
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751..1611
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; LOCATION:
US-08-358-117-1
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1.6%; Score 37; DB 3; Length 2058;

Query Match

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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENITON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENITON: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: S674
SEQ ID NOS: S674
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Best Local Similarity 53.9%; Pred. No. 0.83; Matches 76; Conservative 0; Mismatches
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Pred. No. 1.8;
0; Mismatches
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10.5-09-134-010C-928/c
7. Sequence 928, Application US/09134001C
7. Patent No. 6380370
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Best Local Similarity 51.6%;
Matches 81; Conservative
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